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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
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No.
                                                                                                             May 17, 2000, 04:39:02; Search time 1878.33 Seconds (without alignments)
-1517.972 Million cell updates/sec
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1 cgcggacaagccttggaaga.....aaatggcgatagatattccc 2931
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                  882769 seqs, -486395729 residues
                                                                             OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Direct Submission
Submitted (11-MAR-1998) Environmental Science, Policy and
Management, University of California, 201 Wellman Hall, Berkeley,
CA 94720-3112, USA
Location/Qualifiers
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                       AF053411 2931 bp mRNA PLN 12-SEP-1998 Feus distichus vanadlum bromoperoxidase mRNA, complete cds. AF053411 GI:3582762
                                                                                                                 Eukaryota; stramenopiles; Phaeophyceae/Xanthophyceae group;
Phaeophyceae; Fucales; Fucaceae; Fucus.
1 (bases 1 to 2931)
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Best Local Similarity 100.0%; Score 2931; DB 8; Length 2931;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2931; Conservative 0; Mismatches 0; Indels 0;
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/db_xref="taxon:3012"
/dev_stage="2.cell embryo"
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421 agcrrchaCagacagchrrATCGGCTrCCAGAATCTGGGTRAAATTATGGCCAGGGTCC 480
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HALOPEROXIDASE GENE AND ITS UTILIZATION
nc. JP 1998248581 A 22-SEP-1998;
Corallina piulifera
TP 1998246581-A/1
22-SEP-1998
106-MAR-1997 JP 1997070539
106-MAR-1997 JP 199870870539
101MI YOSHIRAZU, TANABE TADASHI
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Matches 203; Conservative , 0; Mismatches 204; Indels 6; Gaps
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/db_xref="taxon:32644"
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mi, Y. and Tanabe, T.
HALOPEROXIDASE GEN
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Submitted (0.2-21-1996) to the DDBJ/ENGL/GenBank databases. Tadashi
Fanabe, National Cardiovascular Center Research Institute,
Department of Pharmacology: Fujishiro-dai 5-7-1, Sulta, Osaka 565,
Japan (E-mail:tanabe@ri.ncvc.go.jp, Tel:06-833-5012,
Fax:06-872-8092)
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npopontdpsplasftkglpeddngaiidpddflafvrainsgdekbililgpard
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INALXLAALGRELEFSEPDSFRAETIQFALDOLNGLEWFYPAKLADPPAEIRRRG
ETVUGNLFRGILDFGSFOFPLEGY. TIVGSROIGSATVGNRTLYSPNAEPDSFDGELATG
STIISORYRIAFFGERDFYFLKYFLDVQDAADFRGFESYEFGARLIRTIRDLARWHH
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IKANYR OKENIHERLPREATGGLISVWKIAROPKGESIPPEVDLAVEELGDILEKAEIS
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DQVPEDVROEDKIVKSSFKGTLTVAGGELMKLADNIAIGRNAAGYHTFSDQPESLLIGE
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Corallins plulifera mRRA for vanadium-dependent bromoperoxidase 1,
complete cds.
1796 ccaagigggatcgccaacgcacccttcctacccgtccggccacgctacccaaaatggagc 1855
1419 ccccaadgcacccarrccarccarccaracgcaacgccacccaracgcaccc 1478
                                                                                                                                                                                                                    1856 atttgccacagttctgaaggccctcattggcctagatcggggaggtgagtgcttcctaa 1915
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Shimonishi, M., Kuwamoto, S., Inoue, H., Wever, R., Obshiro, T.,
Iluni, Y. and Tanabe, T.
Iluni, T. and Tanabe, T. and Tanabe, T. and T. and
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/protein_id="BAA31261.1"
/db_xref="G1:3293050"
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Corallina pilulifera CDNA to mRNA, clone:BPO1.
Corallina pilulifera CDNA to mRNA, clone:BPO1.
Corallinaceae; Rodophyta; Florideophyceae; Corallinales;
Corallinaceae; Corallinoideae; Corallina.
Tanabe,T.
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/db_xref="taxon:78447"
/clone="bpol"
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2.2%; Score 64.6; DB 7; Length 2 Similarity, 49.2%; Pred. No. 8.7e-07; Indels 3; Conservative 0; Mismatches 204; Indels
OVAIGILEBOSLTYGENFFFNLPKFDGTTIQI"
544 c ! 552 g 488 t
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Submitted (02-SEP-1996) to the DDBJ/EMBL/GenBank databases. Tadashi Tanabe, National Cardiovascular Center Research Institute,
Department of Pharmacology, Fujishiro-dai 5-7-1, Suita, Osaka 565,
Japan (E-mail:tenabe@ri.ncvc.go.jp, Tel:06-833-5012, D97659 2029 bp mRNA PLN 07-JUL-1998 Corallina pilulifera mRNA for vanadium-dependent bromoperoxidase 2, Complete cds. D87658 1 GI:3293051 1839 1486 GCAGAACATACCTGACGGAGATCCTGACCCTGATCCTTCATTCCTGTTGCCGATGCCATT 1545 1606 ATCTCTCACGATCCTGAAGGCGTTCTTCGACTCC----GCCATCGAGATCGATCAGGT 1659 1720 TGTTGCCGGTGAATTGAACABGCTCGCCGACAATATTGCGATCGGCGCTAACATGCCAGG 1779 1796 ccaagtgggatcgccaacgcaccettcctacccgtccggccacgctacccaaaatggage 1855 1856 atttgecacagitetgaaggeeeteattggeetagateggggaggtgagtgetteeetaa 1915 2 (bases 1 to 2029)
Shinonishia, Kuwamoto, S., Inoue, H., Wever, R., Obshiro, T.,
Shinonishia, Y. and Tanabe, T.
Cloning and expression of the gene for a vanadium-dependent
bromoperoxidase from a marine macro-alga, corallina pilulifera
PEBS Lett. 428 (1-2), 105-110 (1998) 1660 GTTCGAGGTCGACAAAGATGAGGACAAGCTTGTGAAGTCGTCTTTCAAGGGAACTCTCAC ccccgtgttccccaagcgatgacggcctggaactaatcaacttcgaagggggcatgccttac catecactateggttegaeggtateeaaggeetaetteteggagagaeaateaetgtaeg 1780 Terreacraciforeagricastreserreicies de activitation de la contractation de la con 2096 aacacttcaccaggagctgatgacgttcgccgaggaagccacctttgaattcc 2148
1840 AarcTrggAagaAcacaAaActcrcAcararGcGGAGAACTTCTTCRACTAGC 1892 9 Length 2035; vanadium-dependent bromoperoxidase 2.
Corallina pilulifera CDNA to mRNA, cione:BPO2.
Corallina pilulifera
Corallina pilulifera
Corallinaceae; Corallinoidese; Corallinales;
[ (pages 1 to 2029) nabe, Matches 203; Query Match Best Local S

/organism="Corallina pilulifera"
/db\_xref="taxon:78447"
/db\_xref="taxon:78447"
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/codon="start=1"
/product="vanadium-dependent bromoperoxidase 2"

Location/Qualifiers 1.:2029

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06-MAR-1997 JF 1997070539
IZDAT YOSHIKAZU, TANRAE TADASHI
Cl2N15/09,Cl2N9/08,CL2N15/09,CL2N1:89),(Cl2N9/08,Cl2R1:19);
Strandedness: Double;
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                                                                                                                                                                                                                                                                                                            /organism-'Corallina pilulifera' FT
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Location/Qualifiers
1..1791
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Corallina pilulifera
JP 1998248581-A/2
22-SEP-1998
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HTG: HTGS_PHASE2.
fruit fly.
                                                                                                                                                                                                   topology: Linear;
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LYEAFLINACLILLANGYPEPARLEPGOBKLUHHDFYWRGARVLILTUTEANTRALK
AVRYOKFHTHREAPEANGGLISVHKKSFLAGSDIIFPEYSELVEELSSILLDVAKESN
EKONRADGIVSPOKSFLLPWARAEGSPFHPSYGGGRAVVAGACTTILKAFTDANFQIO
KVFEVDTDEDKLYKSSFKGTLYVAGELKKLADNYALGRNWAGVHYFSDOFFSLLLGFO
IAIGILESGLIYGENFFWLFPDGTTIQI
                                                    /tradslation="MGIPADNLOSRAKASFDTRVAAAELALARGVVPSFANGEELLYR
                                                                                                      iglp iwrsdlanslelevrgwenssagltfolegpoaosvamppapylmspeliaema
                                                                                                                                                                  IVGNLFRGILPGSEVGPYLSOYIIVGSKOIGSATVGNKTFVSPNAADEFDGEIAYGSI
                                                                                                                                       elylmalgrdiefsefespknaafirsaierlnglewfntpaklgdppaeirrrrge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%; Score 63.8; OB 7; Length 2029; Best Local Similarity 46.8%; Pred. No. 1,4e-06; Matches 240; Conservative 0; Mismatches 267; Indels 6;
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Corallina pilulifera mRNA for haloperoxidase.
E17200
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Trumi, I. and Tanabe, T.
Perent: JP 1998, 4881-A 22-SEP-1998;
OTSURA PHARNACEUT CO LID
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'protein_id-"BAA31262.1"
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JP 1998248581-A/2.
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ength

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contig of 1787 in length
gap of unknown length
contig of 592 in length
gap of unknown length
contig of 341 in length
spap of unknown length
spap of unknown length
contig of 1605 in length
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contig
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                                                                                                                                                                                                        Note that the sequence was identified as CDM:10211374 by the submitter. Or further information on this sequence e-mail to fly@celera.com.NOTE: This is working draft's sequence. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is a working draft, sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finishe sequence. I 804: contig of 804 in length 1802: contig of 978 in length
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Drosophila melanogaster chromosome X clone BACR37M19 map 10E stre
Y: cn bw sp, *** SEQUENCING IN PROGRESS ***, in unordered pieces-
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Submitted (14-DEC-1999) European Drosophila Genome Sequencing
                         Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Insecta;
Berryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidas; Drosophilidae; Urosophila.
1 (bases 1 to 28043)
Adams, M. and Venter, J. C.
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                                                                                                                                                 Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, NSA
This sequence was identified as CDM:10211374 hv *be ...-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.4%; Score 41.4; DB 42; Length 28043;
Best Local Similarity 54.2%; Pred. No. 3.3;
Matches 84; Conservative 0; Mismatches 71; Indels 0; Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quencing the X chromosome of Drosophila melanogaster
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:oidea; Urosophilidae; Drosophila.
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/db_xref-"taxon:7227"
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  Drosophila melanogaster
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RTG: HTGS_PHASE1.
fruit fly.
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(bases 1 to 75282)
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0; Gaps

7102 others

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Applantansferase: APP-dependent helicase: dapF: diaminopimelate apimerase: hydrolase: Kinase/phosphohydrolase: laxA; nrdJ: secreted hydrolase: SOS regulatory protein LexA; transcriptional regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ced (24-MAR-1998) Streptomyces coelicolor sequencing project,
Centre, Wellcome Trupus, Hinkton, Cambridge
NA E-mail: bernell@sanger.ac.uk Cosmids supplied by Prof.
N. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinorycetales; Streptomycineae; Streptomycetaceae; Streptomyces
1 (bases 1 to 3840)
Seeger, K.J. and Harlis, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W.sanger.ac.uk/Projects/S_coelicolor/) CDS are
the following system e9 SC787.01c. SC (S.
77 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                   Db 19436 CGATGGACTTGGCCGGATGCCAAATCTGCTCCGGGTGCACCTGCATCCCGATCTTGGCGA 19495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                f ordered cosmids and a detailed genetic and physical map is 8 Mb Streptomyces coellocalor A3(2) chromosome crobiol. 21 (1), 77-96 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                         Db 19496 AGAGITIGACGCACIGCICGGACGIGCGAACGCIGTIGTIGGICAGGAAGGICAGAIGCI 19555
                                                                                                                                                                                                                                                                                         1088 cgctggaatgggaggcttcccaaatctggacgccgtgtcgatagggtccgatggtacggt 1147
                                                                                                                                                                                                                                                                                                                                                                                 1148 ggaccogttctcccagctcttccgagcgaccttcgttggtgttgaaacggggccctttgt 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 38400)
edenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
inashi, R. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane efflux protein; tRNA delta(2)-lsopentedflux proteinsphate transferase; two-component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                Score 41.4; DB 32; Length 75282;
Pred. No. 3.9;
0; Mismatches 71; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Apr 8, 1998 this sequence version replaced gi:2995287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.to 38400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19556 TGCCCATCTGCTCGAGAGCGCCATATCCGTCGGCG 19590
                                                                                                             14540 c 14571 g 19191 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1208 ctctcagctgctcgtgaacagcttcaccatcgacg 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norwich, Norfolk NR4 7UR, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SC4R2 38400 bp DNA
Streptomyces coelicolor cosmid 4H2.
AL022268
/clone-"BACR37M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor A3 (Streptomyces coelicolor A3 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268.1 GI:3036873
                                                                                                                                                                                                Query Match
Best Local Similarity 54.2%;
Matches 84; Conservative
                                                                                                                19878 &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
ACCESSION
VERSION
REYWORDS
                                                                                                          BASE COUNT.
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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JOURNAL
REFERENCE
AUTRORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JODRNAL
MEDLINE
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Drosophiia melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This record will be updated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .75282
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gap of unk
contig of
gap of unk
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contig
gap of
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contig
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06-APR-1998

BCT

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/db_xref-"SFTREMEL:069958"
/translation="markylleredelilgideligheragryrispaglyddarge
/ggllplgaseeryagarighillidalgeleytasblythikshypaglyddanyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a<u>ooloysaavgaflygialsgevaegahtllsplirdlfaavffvf</u>
Tlepalalalltavtkiatgymaarragisykgrwraggalvarge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tradslaton="maaprigatplegigyodlyyrerrhisyvahrdgrywyyr
Sddpdscahislaligeragalidalkepshesasllyttdleinarrievaatsrwgr
Ligdprriptogstynyvlrrrraraiebeardprivggdtlytgtregydaaligg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSIVIAGLAVSAGIEPSLGPLATAYVLILVVLGPLTARFTEPLAMRLFPRRDNPDRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHDEVGQTLTAVLLQLKRVADRVPGELRDEVTLAQEATRAGLDETRRIARRLRPGVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elglasalrslaaefthhgltvqhhipgdlpplapeaelvlykvaqegltntarhad/
                                                                 protear, Sckii. 03c, possible transmembrane transport protean, u.e., 411 as, similar to several hypothetical proteans eg. M. tuberculosis TR:005831 (EMBL:255121) Proteans eg. M. tuberculosis TR:005831 (EMBL:255121) MTCT20811.11C (365 as), fasta scores opt: 1226 2-score: 1612.0 E(): 0, 53.5% identity in 372 as overlap, and to members of the REFENTER potassium transporters family eg. KERE_ENCOL P4552 glutethione-regulated opt: 32538 identity in 396 as 2-score: 292.9 E(): 4.3e-09, 25.3% identity in 396 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * two-component sensor protein,
nany e.g. DEGS_BACSU B13799 sen,
. Bacillus subtlis (385 aa).
score: 334.6 E(): 2e-11, 31.3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u> AGLVVATALLLGPVTVSTPVLAGEAL</u>VLLAGLAALLAGNAVVLRIGLTPLHRLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOD - MGVVTDIRSRSRSAKLAAGVSCEKAGRSGKRNVSLFWRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-'putative transmembrane transport protein" /protein_id="Cal8319:1" /db_xref="G1:2995290"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical proteins from several organisms e.g. m
tuberculosis TR:00582 (Embi:05121) MTC/2051.12C
ma), fasta scoras; opt: 315 z-score: 557.4 E/): 6-
40.0% idelativ in 150 ma overlap (also upstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3014. .3018)
//gene="Spirity."
//gene="possible RBS upstream of SC4H2.03c"
complement(3506. .3509)
//orde="possible RBS upstream of SC4H2.04c"
3602. .3506
//orde="possible RBS upstream of SC4H2.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product='Aypothetical protein SC4H2.04c'
/protein_id="CAA18320.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -"putative two-component sensor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3611. 4687. /gene"Schel.05. probable two lone. 3542.05. probable two len: 358 as; similar to many protein degs (ec 2.73..). 88 fasts scores; opt: 317 z-scoredidentity in 227 as overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative transport protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"SPTREMBL:069959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="G1:2995292"
/db_xref="SPTREMBL:069960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SC4H2.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3011. .3496)
/gene="SC4H2.04c"
complement(1771. .3006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLAEGTPRAAATEEASVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SC4H2.05"
3611. .4687
                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         table-11
                                                                                                                                                                                                                                                                                                                                                                                                      overlap
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                                                         are also intrinced but some of these may be forthfolds. The tength in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Kropp et al., Nucleic Acids Research, 22(22):4/68-4/78(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at.

http://www.inh.go.jp/
lun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon of acts) with a preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most important in sequence of in may be shorter because we arrange for a small overlapping sections once, or longer, because we arrange for a small overlapping sections once, or longer, because we arrange for a small overlapping section once or longer. Statis and Stabs.

Location/challifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SC4H2.01c, probable secreted protein, len: 331 aa; some similarity toa secreted protein from Brucella abortus BCSP_BROAB P12920 31 kd immunogenic protein precursor (329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttedblaton="mstllsrigerravoctvagavvicillmmilplgekppsgtit
Stgtragvyokygellrtelrkdmpgidyrlmtsrgsognyervasgeadftiaaad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIATRILRAVGIDPETDITPRADGIDTGPGRLGDELDAFFWSGGVPTDGLREIAESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - MAVATWYGMSSIPPAESGPPSAEGRIPPDQGRISPDQGRISPAD
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPRLITEWLI RIVLDSRDGIGARVHSAQLVDLRTALITDPLELHEGARRITRSVKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="overlap with Cosmid SC4E8 from: 15450 to: 15560"

complement(91. 1086)
/gene="SC4E2.01c"
complement(91. 1086)
/gene="SC4E3.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1136. .1675
/gene="SC4H2.02"
/note="SC4H2.02, unknown, len: 179 aa; Proline-rich in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aa), fasta scores; opt: 399 z-score: 357.4 E(): 1.1
32.7% identity in 336 aa overlap. Contains probable
M-terminal signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1095. .1098)
/note="possible RBS upstream of SC4H2.0lc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Streptomyces coelicolor A3(2)"
/strain-"A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product = "hypothetical protein SC4H2.02"
protein_id="CAA18318.1"
db_xref="G1:2995289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roduct-"putative secreted protein"
rotein_id-"CAA18317.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"SPTREMBL:069956"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:100226"
/clone="cosmid 4H2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene-"SC4H2.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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gene

FEATURES

CDS

gene

CDS

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/gene="Scc88.01"
//gene="Scc88.01"
//gene="Protein sequence is in conflict with the conceptual
translation; SCG88.01 posaible glycosyltransferase, len:
-1.135 ag; N-Erminal region similar to TR:03XC92
(EMB:AR146523) Riebsiella pneumoniae glycosyltransferase,
329 ag; fasta scores: opt: 214 z-score: 245.4 E(): 3e-06;
-1:38 identity in 263 ag overlap and c-terminal region
similar to SW:TAGF_BACSG (EMB::315200) Bacillus subtilis
teichoic acid biosynthesis protein F TagF, 746 ag; fasta
acores: opt: 1056 z-score: 1203.0 E(): 0: 41.5% identity
in 381 ag byerlap*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.nih.go.jp/
lun/cgi-lan/framepidt.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream tibosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codous its given for each CDS.

The length in codous is given for each CDS.

The bost is the highest scoring match found by fasts — o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons Nucleic Acids Research, 22(22):4768-4778(1994), and the FramePlot program of Eibb et al., Gene 30:157-66(1984) as implemented at
        Submitted (14-FEB-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Minxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwaco, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UB, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESLDESGSDFVTGNVQHINSTKIWQSPNHRILAGGAVRRTHISRNKLLIDRIACNKV
FRREPREKRIDLSPPECVLLEDVPVILDAQFLABANDIISBPFYVRLREGBABSTYO
RRIEDRAKRBDAAMSENSKERSRPGESGABLKHAYDHIALTGDLRIFLNVLDPGDA
EFRAEFLRVINKYLLQVDPRVVMELPATRHILAVRHALDDLVDLIKAERGDDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFRAEFLRVINKYLDQYDDRVVMELPATARIKWLLVRKHALDDLVDLIKAERRGDAVK
ISGLVRKYVSYPTVEAAAAGLPKKARRIDPDLRLHAPLODIRWDGGRLRLSGHAWVDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MRKENAGLGAARNTGMTRLAPESEYVAFVDSDDMIPPDAYRLM\
                                                                                                                                                                                                            Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Becwilf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Mide Web.
(URL: http://www.apager.ac.uk/Projects/S_coelicolor/)
CDS are numbered Using the following system eg SC787.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   important: This sequence MAX NoT be the entire insert of the sequence clone. It may be shorter because we only sequence overlapping aections once, or longer, because we arrange for a small overlap between neighbouring aubmissions.
Cosmid CBB Liess between and overlaps with cosmids C123 and C80 on the Aser: genomic restriction fragment.
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/protein_id-"CAB75371.1"
/db_xref-"GI:6983732"
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/clone="cosmid C88"
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araaltlepedagvellyrddgtgelgtaabgagtrgmreralligaethfepapgg
stdvrlhvpappgdrcadrtgdsp"
                                                                                                                                                                                                    /note="SC4R2.06, probable two-component transcriptional regulator, len: 219 as, similar to macy e.g. DEGL_BACSU P13800 transcriptional regulatory protein degu (229 as), fasta acores; opt: 343 z-score: 736.1 E(): 0, 37.14 identity in 224 as overlap. Contains PS00622 Bacterial regulatory proteins, luxR family signature, Pfam match to
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50S ribosomal protein L27;
50S ribosomal membrane protein; mreB; mreC; mreD; ndk; obg;
50S secreted protein; sfr; transferase; valS.
51reptomyces coelloclor A3(2)
51reptomyces coelloclor A3(2)
52reptomyces coelloclor A3(2)
54reptomyces coelloclor A3(2)
54reptomyces coelloclor A3(2)
55reptomyces coelloclor A3(2)
56reptomyces coelloclor A3(2)
57reptomyces coelloclor A3(2)
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Redenbach, W., Kleser, H.M., Denapaite, D., Bichner, A., Cullum, J.,
Klanshi, H. and Hopwood, D. A.
A set of oxferred cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mich. Microbiol. 21 (1), 77-56 (1996)
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Unpublished
3 (bases 1 to 42816)
Cerdeno, A. w., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
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llarity 44.2%; Pred. No. 12;
Conservative 0; Mismatchea 206; Indels 0;
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/gene="SC4H2:06"
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/ Anote="SCC88.03c"
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/product="putative transferase"
/db_xref="GI:698734"
/translation="MKITFLIFWGDEMGGTEQAVYTQATHLAPRHDISVLSVFKTREQ
TLSAADGAHTPFTVRVPMRDVALLPËHQDYVKEENAAGGADPAAASRRNWSTOLVAVA
PDGGERRFSTVVREGLADGEMRLPASLAENADRNETALVSGHNGYLKFSGRPLDAKIT
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Protein_id="CAH75372.1"
/db_xref="G1:6983733"
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/trasiation-wkolptpboynrkgyanyrsarskidslyuyppspddwrryadd
Hislidgrilanycytypddliaasaslyigggsspyviplinggrenslandrsvy
Dilenyrdsspyphomerellengchrisytyddrggrenslandrprimpedpti
Pepyrndgyrchytasyrgralisigndraniisydydigwsgytlrggrinyrsarac
SGDVELIRRKGKYSRTLPATWGGDVFTCTVHTADFGASGSKEQIMDVRLRRPRGRSL
LCRRRPRDYRSGDVFRRPRRLIADGGTALRHPYTTPVGSLAFRAALIPSGS°
/gene-"SCC88.05c"
                                                                     aaaknnralleerrgytvansfyhaprelresyles ieedfpesyvrtaatphrcwod
smysslhhygyltogsydssircatdogtysrhpeltrllamrchdyfclgesod
GAORFFLANGASRFFWSPTTVPVGEPTEEDEGYE
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Home saplena chromesome 4 clone RF11-440L14 map 4, WORKING DRAFT
SEGUENCE, 20 unordered pleces.
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Eurheria; Frimates; Catarrhini; Rominidae; Homo.
1 (bases 1 to 18875)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-440L14
                                                                                                                                                                                                                                                               complement(7124. 7570)
/gene="scU88.03c"
/notes"Pfam match to entry PF00534 Glycos_transf_l,
Glycosy transferases group 1, score 99.70, E-value
2.1e-27.
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/protein_id="CAH75374.1"
/db_xref="GI:6983735"
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/gene="SCC88.04c"
/note="SCC88.04c, unknown, len: 329
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1.3%; Score 38.6; DB 2; 19est Local Similarity 51.4%; Pred. No: 21;
Matchea 89; Conservative 0; Mismatches 84;
                                                                                                                                                                                                                AEVPEREGARIVEAFLRAYFPVKSPYER
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RTG; RTGS_PHASE1; RTGS_DRAFT.
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Macdonald, P., Marguls, N., McEvan, P., McGurk, A., McKernan, K., McPherers, R., Meldtim, J., Meneus, L., Morrow, J., Maylor, J., Morrow, J., Maylor, J., McMorrow, J., Maylor, J., McMorrow, J., Maylor, J., McMorrow, J., Maylor, J., McMorrow, J., Stanger, R., Severy, P., Spencer, D., Stanger, Thoman, D., Stojanovic, N. Subramalan, A. Talamas, J., Teafaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Myman, D., Ye, W. J., Direct Submission
                                                                                                                                                                             Submitted (27-7AN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 1, 2000 this sequence version replaced 91:6778502.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13, M77815, 100% of reads Sequencing vector: M13, M77815, 100% of reads Assembly reversing the program: phrap: version 0.960731 Consensus quality: 178202 bases at least 040 Consensus quality: 18602 bases at least 020 Insert Size: 188975; aum-of-contigs outlity coverage: 4.2 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                         web-site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome:wi.mit.edu
Center project Information
Center project name: 15090
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s 1 (Dases 1 to /205)
s 2 (Dases 1 to /205)
s 3 (Dases 1 to /205)
s Anderson S. Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campoplano,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cocke,P.,
DeArellano,K., Dewar,K., Dodgs,S., Domino,M., Doyle,M.,
Senestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Plerre,N., Grant,G., Hagos,B., Heaford,A., Borton,L.,
Kiein,J., Landers,T., Largocque,K., Jones,C., Kann,L., Karatas,A.,
Kiein,J., Landers,T., Largocque,K., Lehoczky,J., Levine,R.,
Lieu,C., Lilu,G., Locke,K., Macdonad,P., Macquis,N., McCran,D.,
McRan,P., MGuth,A., Miranda,C., Mlenga,V., Morrow,J., Maylor,J.,
Norman,C.,H., O'Conno,T., O'Donnell,D., O'Nivar,T.M.,
Peterson,K., Pleare,N., Pleani,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 126447 CAGTCCCAGGGGGGGGCCCTTCCCACCGGGGGCTCGCCCCAAACCGGGTGGAGGG 126388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 126387 GGTGGGGGGGGGTGCAGATCGCGGCGCTTCCCTGCCCTCTGGCCCTGTGAGACTCCAC 126328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 126327 CGCCCACCCCACCTCCCGGTAGCAGAGGGCAGAAGCAGAGCAGACGTTTCCTCTGCAGACA 126268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy 1009 actggatggcgctggccagggatgtaccctttatgcagtatggcaccgacgaaattacca 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oy 1069 ctaccgcggcagccaacctcgctggaatgggaggcttcccaaatctggacgccgtgtcga 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             949 caataccccoggtacctacccttcctctqagctcgccgctcagttggcggagctat 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 38.2; DB 52; Length 188975;
48.4%; Pred. No 34;
tive 0; Mismarches 113; Indeis 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazod) Chordata, Craniata; Vertebrata, Mammaila, Eutheria, Primates, Catarrhini, Rominidae, Homo.
1 (bases 1 to 72683)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo saptens chromgsome 7, clone Rpii 589F23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACUSSOS 12683 bp DNA HTG 15-FEB-200 SEQUENCE SAMPLING
105422: contig of 13479 bp in length gap of unknown length 125385: contig of 19963 bp in length 42244: contig of 16859 bp in length gap of unknown length 188975: contig of 16859 bp in length 188975: contig of 46731 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_"RP11-440L14"
/clone_11b="RPCI-11 Human Maie BAC"
39301 a 50808 c 53913 g 44948 t 5 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D 126267 TCGGGGAGGTGGGGTCAGGGCCGCGGGTTCCAGCCCT 126229

    Qy 1129 tagggtecgatggtacggtggacccgtteteccagetet 1167

                                                                                                                                                                                                                                                                                                                                /organism="Homo saplens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                Location/Qualiflers
1. 188975
                                                                                                                                                                                                                                                                                                                                                                                                         .. /chromosome-"4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 48.48
Matches 106; Conservative
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TITLE JOURNAL COMMENT

19020 19944: contig of 925 bp in length	ity of 919 bp	15 of 910 b		gnp of unknown length 22687 23617: contig of 931 bp in length	gnp of unknown length 23618 24528: contig of 911 bp in length	gap of unknown length 24529 25425: contig of 897 bp in length	gnp of unknown length contig of 926 bp in 1	gap of unknown length 26352 27273: contig of 922 bp in length	gap of unknown length 27274 28210: contid of 937 bp in length	gap of unknown length 29139: contig of 929 bp in 1	gap of un) 30047: contiq of	gnp of unknown length 30908: contid of 861 bp in 1	gap of unknown length	31830: contig of 922 bp in 1 gnp of unknown length	31831 32733; contig of 903 bp in length que to take the same of taken length	19 of 896 b	19 of 883 !	19 of	of unknown iig of 870 b	9ap of unknown length 36309 37230; contig of 922 bp in length	gap of unknown length 37231 38157: contig of 927 bp in length	gap of unknown length 39069: contid of 912 by in 1	gnp of unknown length	gnp of unknown length	41801 CONTROL OF SER PRINCIPLE	gap of unknown length	gap of unknown length	gnp of unknown length	g pp of unknown femth	gnp of unknown length	TOTAL TOTAL OF THE OF T	on the control of the	48204: contig or 935 bp in 1 gap of unknown length	49085: contig of 881 bp in 1 gap of unknown length	49990: contig of 905 bp in 1 gap of unknown length	50894: contig of 904 bp in l gap of unknown length	51781: contig of 887 bp in gap of unknown lengt	. 51782 52679: contig of 898 bp in length
* *	* *			* *	* *			* *	* *	**		* *	* 1	• •	* *	* *	* 1	• •	* *		* *		* *	* *	* *	* *	* *	* *	* *					*.*	* *	* *	* *	* 1
N., Tirrell.A.	Wilson, B.,		r for Genome		<b>.</b>	e Research												•															• .			•		
Severy, P., Spencer, B., Stange-Thomann, N., Stojnnovio, Subramanian, A., Talamas, J., Tesfave, S., Theodore, J.	Mi.X. Wuman D. Ye W. J. Vound G. Paincin J. Filmer B.	/: 0/mpomma /: 0	d Institute/MIT Cer		<pre>Smit, A.F.A. &amp; Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMnsker.html</pre>	Center: Whitehead Institute/ MIT Center for Genom			Center project name: L6506 Center clone name: 589 P 23	NOTE: This record contains 8	* sequencing reads that have not been assembled into *.contigs. Runs of N are used to separate the reads	2.8	identifying clones that may be gene	Overlap retalionships among clone However, it should not be assumed	will be sequenced to complet the record is updated, the a	* be preserved. * 1 011. contin of 011 by in leasth	dup of unly	gap of unk	2732: contig of gap of unk	3630: contig of gap of unk	4513: contig of gnp of un)	# g	of.	9 5	ğ	of	9978: contig of qap of unk	of un	w 4	ų,	y.	Ą	a o	<b>44</b>	ă ș	<pre># gap of unknown length # 17205 18114: contig of 910 bp in length</pre>	unknown of 905 b	ğ

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50-ST 0002 /2:T2:27 01	-TPT-T8A-T.TGe	Pag
	1	
gap	FEATURES	Location/Qualiflers
퓻 6	source	•
* 53553 54466: contig of 914 bp in length	•	/db_xref="taxon:9606"
3	•	/chromosome="X" /map="X"
8 5	•	/clone="RP3-440021" /clone_lib="RPCI-3"
\$ 56296 57215: contig of 920 bp in length	repeat_region	٦\
* 57216 .58155: contig of 940 bp in length	repeat_region	3311332 /hote="11 repeat: matches 4392 5390 of
* 58156 59072: contid of 917 ho in length	repeat_region	11792209 /notes#film3 monet: metabor 1 1051 of
to day.	repeat_region	2917. 3215
to dap of unit	repeat_region	/note="AluSx repeat: matches 5302 of 36683877
one/s contro of anymown 16	repeat region	/note="MIR repeat: matches 247. 41 of consensus" n 49935216
61785: contig of gap of un)		/note="Alux repeat: matches 301. 80 of consensus; incomplete repeat"
* 61786 62664: Contig of 879 bp in length	repeat_region	5239 . 5279
TO BEEN THE PROPERTY OF THE PR	repeat_region	5343. 5789
1.3%; Score 37.5; DB 55; Length 72683; nllarity 52.6%; Pred. No. 43;	repeat_region	/note="MLT2FA repeat: matches 395 7550 7857
Matches	repeat region	/note- A
Oy 2774 tyagagtacctgtaccagtatggtgtaagacatatttttctcctgttatggatctgtaga 2833		/note-"Lifrepeat: matches 48715035 of consensus"
Db 43942 TGAAAGAAAATGGAAGACTTTGGCTGTCTTAAATATACATCCTTGCATCTATTTCCAAA 44001		/note-'MALTSCB repeat: matches 501455 of consensus'
Qy 2834 acagctaggtgttgttttatacacaggatgctataaaatagggatgttgataatggcatc 2893	uor6ar readar	n . 1040610679 /note="MILID repeat: matches 4945 of consensus"
-6	repeat_region	11071 /note="L
	repeat_reglon	16303. 17189 /note=#11583 nonest: matches 1 001 0f
	repeat_region	18419 18722
9	repeat_region	/bote="AluSq repeat: matches 1302 of c 1872921555
RESULT 12	repeat_region	/note="il repeat: matches 25335384 of consensus" n 2141921991
#5440021 LOCUS #5440021 107677 bp DNA PRI 23-NOV-1999	Tebest teaton	/note-"Linci repeat: matches 6549 of consensus" 21995 22287
A sequence from PAC 440021 on ch	1	/note="Alustranger: matches 2881 of consensus"
ACCESSION 284481	repear Tediton	<pre>// / / / / / / / / / / / / / / / / / /</pre>
	repeat_region	2285923715 /note="L1MB6
Σ	repeat_region	2411625064 Anotem#1 renest: matches 4623 3674 of
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria: Primatos: Catarrhin: Rominiana: Homo	repeat_region	75553 . 25452
- REFERENCE 1 (bases 1 to 107677)	repeat_region	25455 26328
Direct Submission	repeat_reglon	/note="L1 repeat: matches 3686. 2779227829
JOURNAL Submitted (17-APR-1997) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mall enquires: humquery@sanger.ac.uk Clone	repeat_region	/acte=15
requests: clonerequest(sanger.ac.uk COMMENT On Apr 19, 1997 this sequence version replaced of 1806016	actions + social	/note-"M]
de Jong P.J., enquires: http://bacpac.med.buffa		/note-"L1
2 2	repeat_region	30949. 313 /note="Lips
15 K	repeat_region	<pre>1 31347. 31698 /note="THELC repeat: matches 2. 371 of consensus"</pre>
annotated numan repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'	repeat_region	31700. :32191 /note="LlMA3 repeat: matches 5011 of consensus"
The true left end of clone 440021 is at 1 in this sequence. The	repeat_region	1 32043 .33837
at	repeat_region	33861. 34173 /hote="AluJo repeat: matches 3011 of consensus"
Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCTPAC2.	repeat_region	3450034538 /note="MIR2 repeat: matches 102140 of

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02 repeat: matches 1074. .1011 of consensus. 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAl3 repeat: matches 903. .353 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te-"MIT2A repeat: matches 295. .453 of consensus"
24 .62683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D1 repeat: matches 957. 839 of consensus"
229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 256. .1051 of consensus
                                                                                                                                                                                                                                                                                                                                                                                   34 repeat: matches 456. 533 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 5297. 3008 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 repeat: matches 4574. .3737 of consensus 47735
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5885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 5390. .4604 of consensus*
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2789
                   consensus
                                                                                                                        note-"LIMA2 repeat: matches 1055. .1 of consensus"
0054. .40932
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0406
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                                                                                                                                                              note-"11 repeat: matches 5390. 4523 of consensus 0973. 41158
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                                                                                                                                                                                                                                                                              repeat: matches 53. .146 of consensus"
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                                                                                     note="MIR repeat: matches 222. .32 of consensus" 9158. .40210
                                                                                                                                                                                                                                                                                                                   repeat: matches 1. .300 of consensus
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                                                                                                                                                                                                                                         repeat: matches 209. .6 of consensus"
                                                                                                                                                                                        R repeat: matches 191. .2 of consensus"
1432
                 repeat: matches 648. .888 of
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                                                    copies of 2 mer 93 % conserved"
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Submitted (28-077-1999) to the DDB/ZMBL/GenBank databases.
Masahira Hattori, The Institute of Physical and Chemical Research
(RAIKEN), Genomic Sciences Center (585); Kitasato Univ., 1-15-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2774 tgagagtacctgtaccagtatggtgtaagacatatttttctcctgttatggatctgtaga 2833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2524 TGAAAGAAAATGGAAGACTTYBGCTGTCTCTAAATATACATCCTTGCATCTATTTCCAAA 2583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2834 acagctaggtgtttttatacacaggatgctataaaatagggatgttgataatggcatc 2893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0000648 151496 bp DNA HTG 04-FEB-2000 mmo sapiens chromosoma 11 clone CMB9-76D16 map 11q14, WORKING CART SEQUENCE, 26 unordered pieces.
                                                                                                                                                                                                                                                                                                 68431. .68552
/note="WIR repeat: matches 70. .211 of consensus"
68633. .68706
/note="LiMA2 repeat: matches 1055. .983 of consensus"
68697. .70419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sukaryota, Metazoa, Chordata, Craniata, Vertebrata: Mammalia,
Sutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                68697. .70419
/note="11 repeat: matches 3804. .2022 of consensus" 70830. .71387
/note="11 repeat: matches 2001. .1428 of consensus" 71389. .>71710. .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .71710 .
                                                                                                                                                                                                                                8226. .68349
note-"WEESA repeat: matches 189. .65 of consensus"
8431. .68552
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Yada,T., Totoki.Y., Watanabe.H. and Sakaki.Y.
151,496 genomic DNA of 11q14
Y in Database (1999) In press.
74118. 74451
/note="MRR22 repeat: matches 1. 345 of consensus"
74959. 74996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog.P.
A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Best Local Similarity 52.64; Pred. No. 46;
Matches 82; Conservative 0; Mismatches 74; Indels 0: 0
                                                                                                                                                                            note-"MITIAl repeat: matches 19. 365 of 8226. .68349
                                                                                                  copies of 2 mer 81 % conserved"
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HIG; HIGS_PHASEL; HIGS_DRAFT.
HOMO Sapiens DNA, Clone:CMB9-76D16.
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DD 88461 TTGGTTGACACTGATCTTGTACTTCCCAGCCCCTÄGAACTGTGAGGAATAATTTCTGTT 88520
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
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27 bp in length
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12 bp
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/Qualifiers
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1.3%; Score.37.2; E
Best Local Similarity 50.3%; Pred. No. 63;
Matches 90; Conservative 0; Mismatches
                                                                                    10686 111200: gap of 3
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camo appiens chromosome 15 cla
EQUENCE, 20 unordered pieces
CO16684
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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685: cont.
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                                                                                                                                                                                    Quality coverage: 4.01x in Q20 bases; sum-of-contigs
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14608 bp in length
                                                                     Sequencing vector: PCR products; 100% of read Sequencing vector: PCR products; 100% of read Chemistry: Dye-terminator ET-amersham; 100% of Assembly program: Phrap; version 0.990329 (Consensus quality: 126527 bases at least 0.30 consensus quality; 13655 bases at least 0.30 consensus quality; 13695 bases at least 0.30 insert size: 139131; sun-of-contigs
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12477 bp in length
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contig of 7528 bp in length
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Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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18: gap of
14298:
                          Center project name: Humbra
Center clone name: CMB9-76Di
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                 Submitted (01-DEC-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                Center: Stanford DNA Sequencing and Technology Development
                                                                                                                                                       Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Bansen, N., Hyman, R., Mao, J., Marathe, R., Horehnuse, A. J., Oefner, P., Palm, C. J., Ramirez, D., Wilhelmy, J., Yu.S. and Davis, R.W.
   Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Bansen, N., Hyman, R., Mao, J., Marathe, R., Horehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Tu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
------- Project information
Center project name: 720
Center clone name: RP11-18H24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exact sizes of the gaps are unknown. It be updated with the finished sequence is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a working draft' sequence. It currently consists of 20 confligs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the confligs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theert size: 165454; agarose-fp
Insert size: 15507; sum-of-contigs
Unality coverage: 4.3x in 020 bases; agarose-fp
Quality coverage: 4.6x in 020 bases; sum-of-con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Vector: Milmpi8; x02513
Chemistry: Dye-primer; 0% of reads
Chemistry: Dye-primer; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 132695 bases at least 020
Consensus quality: 144797 bases at least 020
Consensus quality: 148954 bases at least 020
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Eutherla; Primates; Catarrhini; Bominidae; Ecmo.

    (bases 1 to 156457)

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AUTHORS
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REFERENCE
AUTHORS
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Submitted (09-JAN-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beljing, Beljing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 55114 TTTGCCTGTTTATTGTTTTTTAATTGTGGTAAAATATCCATAATAAAAACGFACTTG 55173
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AC020748/C.
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AC020748 200965 bp DNA
DEFINITION HOMD Saplens chromosome 3p cione RP11-1015N5, WORKING DRAFT
SEQUENCE, 9 unordered pleces.
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karyota; Metazoa; Chordata; Craniata; Vertebrata: Mammalla;
therla; Primates; Catarrhini; Hominidae; Homo
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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20845 GGCGACGCTTAGAGTCCGGCCCGGGCCCAACICCCTCACGGGCCCCCCGGCGGGGGGCAGCGG 20786
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                                                     This record will be updated with the finished sequents soon as it is available and the accession number be preserved.
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b_xref-"taxon:9606"
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Search completed: May 17, 2000, 06:18:16 Job time: 5954 sec

Human Spr5 CDNA. N Mycobacterlophage Lung cancer specif Lung cancer specif	cancer til phos cancer cancer domonas				<pre>encoding cDNA. CP.BP01; CP.BP02; vanadium; halide specificity:</pre>		.se, CP.8P01"	is not indicated"		ding vector, transformed host	me. The haloperoxidase genes 2 are tanjated from Caraltina	h a vector containing the recombinant production of the			6; DB 1; Length 1794: 2e-10;	hes 204; Indels 6; Gaps 1;
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			RES V56	125	KW	FH	FT	FAGG	* <b>* 6</b> 6	8.8		용용			O FA	× 8
GenCore veralon 4:5 lght (c) 1993 - 2000 Compugen Ltd.	- nucleic search, using sw model  May 17, 2000, 04:40:51; Search time 92:13 Seconds (without alignments) 7959.346 Million cell updates/aec	. 8	Gapop 10.0, Gapext 1.0	Total number of hits satisfying chosen parameters: 623170	1000000	Minimum Match 0% Listing first 45 summaries	eq_36:*	Pred. No. 1s tha number of reaults predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score diatribution.	8 Query	ength DB ID Description	1 V56020 1 V56021 1 V74855	1 X07126 Staphylococcus 1 X07127 Staphylococcus	6022 1 V74403 Staphylococcus aur 1012 1 V72124 Human catalytic te 2848 1 V27872 Human telomerase b	1 V27876 Human 1 V22382 Buman	1 V22379 Buman 1 V72125 Human	4023 1 V60320 Human telomerase g 4037 1 V22428 Buman telomerase r 4042 1 V7217 Human catalytic te
Copyrlght	OM nucleic - nucieic se Run on: May 17	Title: US-09- Perfect score: 2931 Sequence: 1 cgcg	Scoring table: IDENTITY_NUC Gapop 10.0, Searched: 311585 secs	Total number of hits sa	Minimum DB seq length: 0 Maximum DB seq length: 1000000	Post-processing: Minimum Match Listing first	Database : N_Geneseq_36:*	Pred. No. 1s tha number of r score greater than or equal and is derived by analysis o		No. Score Match Le	00H		7 34.2 1.2 8 34.2 1.2	34.2	34.2	13 34.2 1.2 14 34.2 1.2 15 34.2 1.2

That cDNA encodes a haloperoxidase enzyme. The haloperoxidase genes encoding the enzymes CP.9801 and CP.8902 are isolated from Corallina pillulifora. A host cell transformed with a vector containing the haloperoxidase genes can be used for the recombinant production of the enzyme. The haloperoxidases of the invention are vanadium dependent and have halide specificity of Donine and iodine. Sequence 1794 Bp; 395 A; 481 C; 505 G; 413 T; 1419 CGCCGAGGCCAGTCCATCCGTCCTACGGAAGCGGCCACGCTGTGGTTGCTGGCGC 1478 1736 ggagatamatgoggogogagatoccaacaacgaggtemeettetteeacaagetat 1795 Db .1359 GCAGAACATAGCTGACGAAGATCCTGACCTGATCCTTCATTCCTGTTGCCGATGGCATT 1418 1796 ccaagtgggatcgccaacgcaccttcctacccgtccggccacgctacccaaaatggagc 1855 1916 occogigitaccaagagatgacggoctggaactaatcaacttcgaaggggcatgccttac 1975 1652 2.2%; Score 64.6; DB 1; Length 1794: 49.2%; Pred. No. 2e-10; tive 0; Mismatches 204; Indels 6; Gaps 1533 GTTCGAGACAAAAGATGAGACAAGCTTGTGAAGTCGTCTTTCAAGGGAACTCTCAC 2.2% Dest Local Similarity 49.2% Matches 203; Conservative ò ò S ð 셤 ò 쉱 . 원

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Claim 2: Pagea 15-18; 20pp; Japanese.
This cDNA encodes a haloperoxidase enzyme. The haloperoxidase genes encoding the enzymes CP. BPO1 and CP. BPO2 are lackated from Corallina pillulifera. A host cell transformed with a vector containing the haloperoxidase genes can be used for the recombinant production of the enzyme. The haloperoxidases of the invention are vanadium-dependent and have halde specificity of bromine and iodine.
Sequence 1791 BP: 390 A; 459 C; 507 G; 435 T;
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09-DEC-1998 (first entry)
Maloperoxidase. CP.BP02 encoding cDNA.
Haloperoxidase; ensyme; CP.BP01; CP.BP02; vanadium; halide specificity:
bromine: iodine: ds.
Corallina pilulifera.
Key
1. 1791
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catccactatoggttcgacggtatccaaggcctacttctcggagagacaatcactgtacg 2095
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                                                                                                                                                                                                                 Ouery Match, 2.1%: Score 62.8; DB 1: Length 1791; Best Local Similarity 46.7%: Pred. No. 7.7e-10; Matches 239: Conservative 0; Mismatches 267: Indels 6.
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"the stop codon is not indicated"
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(SARA) OFGENA PHARM CO LTD.
WPI: 98-560733/48.
P-PSDB: W80551.
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06-MAR-1997;
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PAY Polynucleotide(s) and proteins derived from Staphylococcus aureus - stored on computer readable medium and used in the production of stored on computer readable medium and used in the production of anti-S.aureus vaccines are consistent on the 179-148; 3271pp; English.

Tanti-S.aureus basents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium. preferably selected from a floppy or hard disk, random access medium. preferably selected from a floppy or hard disk, random access medium. preferably selected from a floppy or hard disk, random access medium. preferably selected from a floppy or hard disk, random access of the invention. The DNA sequences allow putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can also be used in a kit for the immunodetection of solved polypeptides can also be used in a kit for the immunodetection of solved polypeptides can also be used in a kit for the immunodetection of shin and surgical wound infections. scaled skin syndrome. toxic shock syndrome etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences contained on the computer readable medium.

The state of any of the saureus DNA sequences contained on the sequence 5280 BP: 2057 A: 744 C; 854 G; 1442 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nuclectide numbering given in the specification for this DNA sequence.
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541. 600
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/*tog= a
/note= *these bases represent a line of missing text in
/note= *these bases represent the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence*
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence.
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Staphylococcus aureus contig SEQ ID #544.
Computer readable medium, vaccine: S aureus infection; immunodetection; cellulitis; eyelid infection: food poisoning: osteomyelitis: therapy: skin infection: surgical wound infection: scalded skin syndrome; toxic shock syndrome: ds.
                                                                     1700 TTGCGATTGGAATCTTGGAGGAGCAGAGGCTGACGATGGCGAGAACTTCTTCTACAATT 1759
teactgtacgaacacttcaccaggagctgatgacgttcgccgaggaagccacctttgaat
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07-JAN-1997. 100117.
05-JAN-1996: US-009661.
(HUMA-) HUMAN GENOME SCI INC.
BARASh_SC, Choi GH, Dilton PJ. Fannon MR. Kunsch CA,
                                                                                                                                                    V74855 standard; DNA: 5280 BP. V74855;
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NPI; 97-374922/35.
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Contain 1 rage 150; 2019; Bugatas, a virulence gene identified in this is the nucleotide sequence of a virulence gene identified in Staphylococcus nureus mutant P11066. S. aureus genes (see X07088-136) associated with virulence were identified by signature-tagged mutanes containing n chromosomal insertion of a signature inged transposon were generated, mutanes with nathence with the management of the mutanes with the nucleotide sequences of the regions flanking the transposon in the nucleotide sequences of the regions flanking the transposon in the nucleotide sequences of the regions flanking the transposon of insertion sites of these mutants were determined. Database sequence comparisons were parformed to identify the virulence genes and to determine the possible function of their protein product (see W97777) is unknown. But the gene is located near to the Opp operon.

W97680-724), The Plic66 virulence gene product (see W97777) is unknown but the gene is located near to the Opp operon.

Comparison search and an antibacterial agent involves assaying potential agents for the ability to directer with the expression of S. aureus virulence gene products. Also new is S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340. gggagaaatcactaggtttcatccaagcgagacgccttatatcnngtacttggaaggct 399
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         535 TCACCATTCAAATGAGTATAACATTGATATAACAGCGCAAAAATATTAACAAATATTACTGC 594
                                                                                       460 gtaaaattatggccagggtccgcatcgctaccgccttggctgtggtactggccgcaccct 519
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                                                                                                                                    595 ATTACAATATATATTTGATGCAGATGTTAAATATATATAGCATTTGGTAATGACCACAATGA 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of S. aureus virulence gene products. Also new is S. aureus containing a functional mutation in one of the virulence genes, and sequence 799 Bp:
                                                                                                                                                                                                                      520 gtttggcattcgacgnggtcacagccagtggtgttttccctgaggancacaagcacac 577
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for, e.g. screening for potential unti-microbial agents
Claim 1; Page 158; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus mutant Pl1G66 virulence gene.
Virulence; Pl1C66; veccine; antibacterial; antibactic;
screening; bacteraenia; oligopeptide transporter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 34.8; D
Llarity 46.6%; Pred. No. 0.56
Conservative 0; Mismatches
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(LMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
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335. .799
                                                                                                                                                                                                                                                                                                                                                                         X07127 standard; DNA; 799 BP X07127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strphylococcus aureus
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Best Local Simi
Matches 111;
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X07127
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Claim 1: Page 155-157; 2030pp: English

Claim 1: Page 155-157; 2030pp: English

This is the nucleotide sequence of a virulence gene identified in

Staphylococcus auteus mutant Plices. S aureus genes (see X07088-136)

English 1: Page 155-157; 2030pp: English

English 2: English 2
                                                                                                      2650 tcaytttggagagtaccgtaggtggcaggacgtatatctctggtagcggtctgttaagaa 2709
                                                                                                                                                         2710 ettecacaagaccgtttacgtttggttgtttagtcgatgcctcttcgttacttgaccgat 2769
                                                                                                                                                                                                                                                             2770 ccattgagagtacctgtaccagtatggtgtaagacatatttttctcctgttatggatctg 2829
                                                                                                                                                                                                                                                                                                                                                                   4098 GIGITGAITGIGGTGCTTCCACTITAGIGGAAGAIAGIGITGICGCGTTTGCTGCTTGCG 4039
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46.6%; Pred. No. 0.56;
Live 0; Mismatches 127; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - useful
      DB 1; Length 5280;
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1.2%; Score 35; DB 1; Length 528
37.2%; Pred. No. 1.7;
Live 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibition of virulence genes from Staphylococcus aureus for, e.g. screening for potential anti-microbial agents Claim 1; Page 156-157; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus mutant Pl1C66 virulence gene. Virulence; Pl1C66; vaccine; antibacterial; antibiotic; screening; bacteraemia; oligopeptide transporter; ss.
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03-JUL-1997; US-887534.
(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
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Best Local Similarity 46.65
Matches 111; Conservative
                           i Similarity 37.2
68; Conservative
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Query Match
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Mntches 68
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1, 97-374922/35.
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Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynoclectide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of
anti-S.aureus vaccines
Claim 1: Page 569-573: 3271pp: English.

Cof the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a fioppy or hard disk, random access medium, preferably selected from a fioppy or hard disk, random access medium, preferably selected from a fioppy or CD-ROM. Romology searches using the S.aureus DNA sequences aliows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therepeutic or indistrial importance can be obtained. Specifically, sequences which are protein-encoded antigens have been identified and these polypeptides can also be used in a vaccine composition against S.aureus infection of the polypeptides can also be used in a fine for a sequence can be used in a variety lifety, eyelid infections, food polsoning, ottor secondablish was production of the polypeptides. The new DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence".
                                                                                                                                                                                                                                                                                                                                                  these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence.
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the sequence listing in the specification, They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence
                                                                                                                  Stabhylococcus aureus config SEQ ID #92.
Computer redable medium; vaccine; S.aureus infection; immunodetection; celluititis; eyeild infection; food poisoning; osteomyeittis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds. Staphylococcus aureus.
655 IAFTGTCATGTTACAACATGCTAGTAGTGGCTAFATTATAGGACCATCAGAAGCATAC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Chol GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                    Location/Qualifiers
421, 480
/*tag= a
                                                                         V74403 standard; DNA; 6022 BP. V74403;
                                                                                                     16-MAR-1999 (first entry)
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07-JAN-1997; 100117
05-JAN-1996; US-009
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This sequence represents a RACE generated fragment of a novel human catalytic telemerase sub-unit (PTC). The hTC protein can be used in screening assays to identify modulators of telemerase and to treat inhibit cellular disorders, death, defects and/or other pathological processes involving telemerase, particularly cancer and ageing (also suitable for this are agents thet stimulate, inhibit or mimic the action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed in vivo. Antibodies and fragments of the protein, used as probes or primers, and may be expressed in vivo. Antibodies and fragments of the protein, used as probes or primers, by (i) detecting abnormal levels of the subunit protein in body fullids or tissues or (ii) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid amount of the encoding sucher acid. Expression of the nucleic acid the ubiquitous expression of the teatomerase RNA subunit.
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Ruman cetalytic telomerase sub-unit RACE-generated cDNA #3.

Ruman catalytic telomerase sub-unit, therapy; dispnosis; hrc; assay; modulator; telomerase subunit, therapy; dispnosis; hrc; assay; modulator; treatment; inhibit; cellular disorder; death; defect; cancer ageing; antidense; neoplastic cell; telomerase-related condition; RACE; qunour cell; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   724 ATTACAATATATATTTGATGCAGATGTTAAATATATATAGCATTTGGTAATGACCACAATGA 783
                                                                                                                                                                           604 GGCACAAATTACAACTATATTAGACGAGCTAGATAAATACCATCAAGAATTGGAAATGAT 663
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                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB) BAYER AG.
Hagen G. Stegmund H. Weichel W. Wick M. Zubov D;
Wali 99-081275/070
New catalytically active subunit of human telomerase - used in the modulation of telomerase activity, particularly for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          520 gtttggcattcgacgaggtcacagccagtggtgttttccctgaggaacacaagcacac 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 34.2; DB 1; Length 10
49.7%; Pred. No. 1;
tive 0; Mismatches BB; Indels
Pred. No. 2.1;
; Mismatches 127; Indels
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6; Fig. 10; 76pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V72124 standard; cDNA; 1012 BP. V72124;
flarity 46.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 49.73
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-1998; E03468.
14-APR-1998; DE-016496.
20-JUN-1997; DE-026329.
26-MAR-1998; DE-013274.
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Matches

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1107 CAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTCTGGG 1166

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1615 tgcatcgatttgcacgccccgaggctctcgggggtaccctccacaacaccatcgc 1669

1167 rrccissocordearsccissorrecessorrecescescersecessos 1221

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Partial convacione 32 codes for a large portion (see W61349) of human relomerase protein 2 (TP2, see W61360), a novel protein of the telomerase complex. It was obtained by PCR amplification (see also V27873-74) of a human colon tumour cell line LIM1863 cDNA.
A 3° sequence was subsequently obtained the LIM1863 cDNA.
A 3° sequence was subsequently obtained (see V27875), and this construction of the clone 32 sequence to obtain full-length cDNA (see V27876) for human TP2 (see W61350). Expressing TP2 genes con a cell is used to increase techomerase activity and thus proliferation for treatment of e.g. HIV infection, AIDS and ageing disorders, while expressing an inactive mutant of TP2 (or molecule antisense to the gene) is used to detrease telomerase activity, e.g. for treatment of cancer. TR2 polypeptides can also be used to serve for agents that inhibit TP2 activity or its binding to TRIP1 (see W61347) or telomerase RNA, potentially useful therapeutically, also to raise specific antibodies useful immunoassays and therapeutically as inhibitors. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding human telomerase protein-2 - used for egulating telomerase activity, e.g. for treating cancer or acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in immunoassays and therapeutically as inhibitors. Nucleic acid fragments are used as diagnostic probes for detecting/quantifying TP2 DNA. Also contemplated are transpenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or they are delivered from
1615 tgcatcgatttgcacgccccgaggctctcgggggtaccctccacaacaccatcgc 1669
                              343 Incagecongearecagearencesecageirecegerisces
                                                                                                                                                      12-OCT-1998 (first entry)
Human telomerase protein 2 (TP2) cDNA partial clone 32.
TP2; human; telomerase protein 2; cancer; AIDS; agelng; therapy;
                                                                                                                                                                                                                                            Iocation/Qualifiers
1920. .2820
/*tag-
/*hote- *this region includes 7 reverse
transcriptase motifs (Claim lb)
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2089. 2820
/*tag- d
/note- (Claim 5)
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/note= "(Claim 5)"
L. .1920
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/note= "(Claim 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune deficiency syndrome
                                                                                                                  V27872 standard; cDNA; 2848 BP.
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WPI: 98-297946/26.
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15-NOV-1996; US-871189.
11-JUN-1997; US-873039.
(AMGE-) AMGEN CANIDA INC.
(AMGE-) AMGEN INC.
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/note- '(C
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engineered cells or gene
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.3-NOV-1997; U21248.
                                                                                                                                                                                                                              Homo sapiens
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The Fuel Man was a controlled and the control of th
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the TP2 gene has been
btides are administered
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                                                                                                                                                                                          Ruman telomerase protein 2 (TP2) full-length cDNA.
TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     662 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as diagnostic probes for detecting/quantifying TP2 contemplated are transgenic animals in which the Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1311 C;
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V27876 standard; cDNA; 3798 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harrington LA: Robinson MO; MPI: 98-297946/26.
                                                                                                                [2-OCT-1998 (first entry
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AMGE-) AMGEN INC.
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3798 BP;
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Matches 87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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DB 1; Length 2848;

Ouery Match 1.2%; Score 34:2; Best Local Similarity 49.7%; Pred. No. 2;

1555 tengattgataggtgeegeegagetggegeagegtgeetegtgttaeesaaagtggeagg 1614

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Fure and recombinant human Telomerase Reverse Transcriptase and 1ts varianty. Watersty.

Fure and recombinant human Telomerase Reverse Transcriptase and in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing Disclosure: Fig. 20: 387pp; English.

Charles and ageing english.

Charles are sequence encodes a human telomerase reverse transcriptase (hTRT) variant from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the charge in hTRT recombinant protein or polynuclectide, on administration of the compound; (B) preparation of hTRT with a telomerase NA compound; (B) preparation of hTRT was a diministration of the compound; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplification product with presence of fMTR in the sample; and (D) carelating the presence of complex or amplification product with presence of thr causes in cell caresing htree capes of a services of a vertebrate cell by increasing htree capes of a product and correlating the complex or amplification of (E) the use of an agent that causes an increase in cell cape of the product and contract a medicament that inhibits the following and the polynuclectic endeading the following and the polynuclectic endeading the following and the polynuclectic endeading the following and t
1108 CAGCTCTCTGAGGCCCAGCCTGACGGCCTCGGAGGCCGTCTTCTGGG 1167
                                                                                                                                                                                                                                                                     13-AUG-1998 (first entry)
Muman telomerase reverse transcriptase Delta182 variant encoding CDNA. Human: telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and the polynuclcotide encoding
medicaments for inhibiting the
of telomerase activity can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag- a /product- "telomerase reverse transcriptase variant"
                                                                     1615 tgcatcgatttgcacgccccgaggctctcgggggtaccctccacaacaccatcgc 1669
                                                                                                        telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            678 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            effect of ageing or cancer. Inhibitors of telemerase activit used to treat conditions that are associated with high telem activity. A protein preparation of MTR can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                avs WH. Cech TR, Chapman KB, Rarley C, Lingner J. OB, Nakannura T, Hariey CB; Rarley C333,76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
56. 2479
                                                                                                                                                                                                                                                    V22382 standard; cDNA; 3855 BP.
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US-911312.
US-912951.
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08-APR-1998.
01-OCT-1997;
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V22382
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The present sequence encodes human telomerase reverse transcriptase the content of the present sequence encodes human telomerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also describes the following methods: A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant content of the compound; (B) protein or polymoricleotide, on administration of the compound; (B) preparation of hTRT with a telomerase by contacting a protein of preparation of hTRT with a telomerase by contacting a protein of preparation of hTRT with a telomerase by contacting a protein of amplifying the product and correlating the presence of complex or amplifying the product and correlating the presence of complex or amplifying the product and correlating the presence of complex or amplifying the product and correlating the presence of complex or increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell research and the polymoric of the presence of ageing the proliferation of hTRT and the polymoric of inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used in preparation of hTRT can also be used in the new entire and in the new horse.
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1096 CAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGG 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human telomerase reverse transcriptase encoding cDNA.
Funan, 'telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                         1615 tgcatcgatttgcacgccccgaggctctcgggggtaccctccacaacaccatcgc 1669
                                                                                                                                                                                                        1156 rrccassccrssarsccasssarrcccsccasscrsccccsccrsccccasscs 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pure and recombinant human Telomerase Reverse Transcriptase and variants are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing Claim 5: Fig.16; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 3955;
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Indrews WH. Cech. TR. Chapman KB. Harley C. Lingner
Colt GB. Nakamura T. Harley CB:
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49.7%; Pred. No. 2.5;
tive 0; Mismatches
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56. .3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V22379 standard; cDNA; 3955 BP
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Best Local Similarity 49.7%;
Matches 87: Conservative
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-PSDB;
                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
V22379
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0; Gaps

88; Indels

Score 34.2; DE Pred. No. 2.4; 0; Mismatches

Query Match
Best Local Similarity 49,7;
Matches 87; Conservative

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DB 1; Length 3855;

1495 gtccattcatcgacagtgatcggcaggcgggcttcgtcaacttcggcacgtctcactact 1554

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04-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a RACE generated fragment of a novel human catalytic telomerase sub-unit (InfC). The hTC protein can be used in screening assays to identify modulators of telomerase and to treat of inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this are agents that simulate, inhibit to mimic the activity of the subunit). Antisense nuclear actis inhibit telomerase action (by binding to specific mank), particularly in neoplastic cells and may be expressed in vivo. Antibodies and fragments of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1063 GACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGGCCCTCCTACT 1122
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1036 GACCAAGCACTICCICIACTCCICAGGCGACAAGGAGCAGCIGCGGCCCTCCTTCCTACT 1095
                                                       1096 CAGCICIGAGGCCCAGCCIGAGIGGCGCTCGAGGCGTCGTGGGGGTCTTCTGGGG 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human catalytic telomerase sub-unit RACE-generated cDNA #4.
Human, catalytic telomerase subunit, therapy; diagnosis; hTC; assay;
modulator; treatment; thiblibit; callulat disorder; death; defect; cancer
ageing; antisense; neoplastic cell; telomerase related condition; RACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (il detecring abnormal levels of the subunit protein in body fluids or tissues or (11) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase RNA subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1495 giccalicategacagigateggeaggeggettegteaactieggeaegicteactaci 1554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New catalytically active subunit of human telomerase : used in the modulation of telomerase activity, particularly for treating cancer
                                                                                                                                                                  1615 tgcatcgatttgcacgccccgaggctctcgggggtaccctccacaacaccatcgc 1669
                                                                                                                                                                                                         1156 TICCAGGCCTGGGATGCCAGGACTCCCGGCAGGTTGCCCCGCCTGCCCCAGGCC 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 11; 76pp; German.
                                                                                                                                                                                                                                                                                                                                                               V72125 standard; cDNA; 3972 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1999 (first entry)
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14-APR-1998; DE-016496.
20-JUN-1997; DE-026329.
26-MAR-1998: DE-013274.
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V60320 ID. V60320 standard; cDNA; 4023 BP.

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The present sequence of the catalytic subunit of a human the present sequence afforms the catalytic subunit of a human telemerase holocargyme. Disruption of the telemerase general alters telemerase not the DNA is assertial for telemerase and a constituted to active telemerase complex. The products can be used for increasing or reducing the lifespan of cells such as cancer cells or transformed cells. They can also be used in the diagnosis and treatment of malignancies. In addition, cells with a longer lifespan can be transplanted into or grafted onto an individual (e.g. as skin and enzymes), to whom they provide therapeutic proteins, such as hormones sequence 4023 BP, 668 %; 1363 C; 1277 G: 715 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1555 teagattgatagtgeegeegagetggegeagegtgeetegtgttaceaaaagtggeagg 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human telomerase catalytic sub-unit gene - used to develop products for increasing or reducing the life span of cells such as cancer cells, or transformed cells Claim 5; Fig 5A-B; 96pp; English.
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49.7%; Pred. No. 2.5:
ive 0; Mismatches 88: Indels 0:
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/note= "refined sequence"
                                                         ubunit; human; telomerase: telomere maintenance:
treatment: cancer; ss.
04-DEC-1998 (first entry)
Human telomerase gene referred to as hEST2
                                                                                                                                                                                                                                                                                                                                                                                 Counter CM, Meyerson M, Weinberg RA;
WPI; 98-495367/42.
                                                                                                                                               Location/Qualifiers
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13-AUG-1998 (first entry)
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/*tag= a
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Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                      US-064322.
US-038750.
US-047151.
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01-0CT-1997; 020890.
                                                                                                                                                                                                                                                                                                         003404
                                                             Catalytic subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSDB; W71376
                                                                                                                          Homo sapiens.
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W09859040-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes human telemerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant to protein or polynuclectide, on administration of the compound; (B) protein or polynuclectide, on administration of the compound; (B) preparation of hTRT with a telomerase NNA cumponent; (C) detection of preparation of hTRT with a telomerase NNA cumponent; (C) detection of preparation of hTRT with a sample by indiging a protein of amplifying the protein or protein in a sample by indiging a regievant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplifying the product and correlating the presence of complex or amplifying the product and correlating the presence of not in the cample; and (D) increasing the proliferation of a vertebrate call by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate call proliferation of hTRT and the polyauclectic effect of ageing or cancer. Inhibitors of telomerase activity can be used in the manufacture of medicaments for inhibiting the cativity. A protein preparation of hTRT can also be used in the new methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pure and recombinant human Telomerase Reverse Transcriptase and its
variants - are useful in the diagnosis, prognosis and treatment of
cell proliferation conditions especially cancer and ageing
Example 1, Fig 74; 387pp; English.
The present sequeace encodes human telomerase reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1615 tgcatcgatttgcacgccccgaggetctcggggggtaccctccacaacaccatcgc 1669
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63. .3461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UTTE-) UNIV TECHNOLOGY CORP. Andrews WH, Cech TR, Chapman KB, Morin GB, Nakamura T, Harley CB; WPI; 98-171633/16.
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172117
172117
AC V72117
DT 24-MAY
DE HUMBN;
KW HUMBN;
KW MODULA
KW MODULA
KW TUMOUL
KW
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Matches
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Claim 4; Fig 1; 76pp; German.

Claim 4; Fig 1; 76pp; German.

Claim 4; Fig 1; 76pp; German.

Chico. The encoded protein can be used in screening assays to identify this sequence encoded protein can be used in screening assays to identify the encoded protein can be used in screening assays to identify the encoders and ageing (also suitable for this are agents that particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunity. Antisense nucles acids inhibit telomerase action (by binding to specific mans, or particularly in neoplastic cells and may be expressed in vivo. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase related conditions (eapecially neoplasta) by (i) detecting abnormal levela of the aubunit protein in body fluids or times are of illy by measuring the amount of the encoding nucleic acid the nucleic acid encoding the aubunit mans is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                  New catalytically active subunit of human telomerase - used in the modulation of telomerase activity, particularly for treating cancer
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1.2%; Score 34.2; DB 1; Leagth 4042;
Best Local Similarity 49.7%; Pred. No. 2.5;
Matches 87; Conservative 0; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1277 G;
                                                                                                                                                          6, Slegmund H, Welchel W, Wick M, Zubov D; 99-081276/07.
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26-MAR-1998; DE-026329.
(FARB ) BAYER AG.
Hagen G, Sierre.
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Sequence
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Search completed: May 17, 2000, 05:50:14 Job time: 4163 sec

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Sequence
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ZIP: 22313-029
COMPUTER RELABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fatenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKER, F. G.
TITLE OF INVENTION: RECOMBINANT FONIPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Foley & Lardner
F: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Petentin Release #1.0, CURRENT APPLICATION DATA: PSPLICATION WIMBER: US/08/232,463 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                 May 17, 2000, 04:39:38 ; Search time 56.46 Seconds (without alignments) 6591:506 Million cell updates/sec
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2931
1 cgcggacaagccttggaaga.....aaatggcgatagatattccc 2931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/FC_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Pc_TUS_Seq:*
7: /cgn2_6/ptodata/1/ina/DaoCxfiles1.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08:463-115-29
US-08-465-388-29
                                                                                                                                                                                                                                                                                                                                                                     226296 seqs, 63486255 residues
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Listing first 45 summaries
                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length DB
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Maximum DB seq length: 1000000
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Perfect score:
.Sequence:
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                                                                                                OM nucleic
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                                                                                                                                        Run on:
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FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPPEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU

LENGTH: 7218 base pairs TYPE: nucleic.acid STRANDEDNESS: single

: IMMEDIATE SOURCE:.; ; CLONE: PT29pt-F1s US-08-232-463-14.

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pair

(703) 683-4109

TELEPHONE: .

6-088-12 5-09145A-12 6-088-14 5-09145A-14

9-12

TELEFAX:

8 8 8

us-09-151-189-1.rni

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                                                                                                  868 cgggagacccggcgggtcgcctcgtcaatcctaccgctgcgtttgccatcgacatatccg 927
                                                        Gaps
Ouery Match
1.2%; Score 36; DB 1; Length 7218;
Best Local Similarity 2.4%; Pred. No. 0.58;
Matches 9; Conservative 208; Mismatches 163; Yndels
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90 Park Avenue
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MENTYON: LS SHUTTLE PHASMIDS
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1356 ttagacgaagagetgegttttateegtaaegeeeggaeetggeeagggteteettegtg 1415
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Pred. No. 8.8;
0; Mismatches 78; Indels
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L5 shuttle phasmid sequence
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                                                                               IGINAL SOURCE:
ORGANISM: L5 mycobacter#cophage
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
15-08-247-901C-1
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Best Local Similarity 50.9%;
Matches 81; Conservative
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INVENTION: LS SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DENTIFICATION METHOD:
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1356 ttagacgaagagetgcgttttatccgtaacgcccgcgacctggccagggtctccttcgtg 1415
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1.2%: Score 34.2; Di
Best Local Similarity 50.9%; Pred. No. 8.8;
Matches 81; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              L5 shuttle phasmid sequence
                                          JMBER: US/09/075,904
May 11, 1998
                    SSOT (ASCII)
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ IO ND:
US-09-075-904-1
                                                                                                          PRIOR APPLICATION OATA:
APPLICATION NUMBER: 08/247,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: L5 mycobacteriophage
OPERATING SYSTEM: MS-DOS
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INDIVIOUAL ISOLATE:
DEVELOPMENTAL STAGE:
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Query Match 1.1%; Score 32: OB 2; Length 704: Best Local Similarity 57.7%; Pred. No. 2.2; Matches 56; Conservative 0; Mismatches 41; Indels
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pilication US/08463115
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OPERATING SYSTEM: IBM P.C. D
SOFTWARE: FASTSEQ VEISION 1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLICATION NUMBER: 07
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F: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.

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1930 CCCTTCTGGGCCCGGCACACCACCACGCTTTCGGGACGAAGCAGCTGGACCAC 1871
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                                                                                                                                     TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICATION NUMBER: US/07/569,781
NG DATE: 23-AUG-1990
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Best Local Similarity
Matches 96; Conserva
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est Pifth Street
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US-08-465-388-29
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RESULT
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Gaps

Indels.

Mismatches 108;

96; Conservative

DB 7; Length 1998;

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Patentin Release #1.0, Version #1.30
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J. BOX 2000, 126 E. LINCOLN AVENUE
                                                                                                               CONSTRUCTION OF INTEGRATIONSCES VECTORS FOR STREPTOMYCES
Application US/08264861A
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                                                       HAIDER
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215 TCCCCCCACGGTNCTCGACGGCCTGCTCCCATAGGGTTGCATTGCGGGTTCCCCATCCC

1817 ccettcetacccgtccggcca

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RESULT 6. 5212296-8/c

1757 teccaacaacgaggteacetacettettecacaagetatecaagtgggate

41; Indels

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1153 cgtteteceagetetteegagegacettegttggtgttgaaacggggeeetttgtetete 1212
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TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
WUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                         pplication US/08959011
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Beat Local Similarity 52.8
Matchea 67; Conservative
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EGRATIVE AND REPLICATIVE EXPRESSION
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Best Local Similarity 52.8
Matches 67; Conservative
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OPERATING SYS
SOFTWARE: Pa
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TELEPHONE:
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                                   INFORMATION
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URRENY APPLICATION DATE: 05/08/276,919
                                                                                              1416 gacaatatcaacaccgaagettatcgcgggtetettate 1454
                                                                                                                                           9495 GECTACACCEACECTTACETCCACGECCEGTCGTACATC 9533
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Torczynski, Richard M. APPLICANT: Bollon, Arthur P. TITLE OF INVENTION: Lung Cencer Marker NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 14
ADDRESSE: RICHARDS, MEDLCK & ANDREWS STREET: 1201 Elm Street, Suite 4500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SISTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           se 9, Application US/08276919
No. 5589579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 80, Conserva
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T5270-2197
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LOCATION:
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-US-08-776-088-12
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                                               281 CCACAAGTCCCGGTCACTCGACCACCAGCGGGGACCTGCTGCTCCCGCCGGTGCCGC 222
                                                                                              cgaggactgcatcttaaacggagatttcagcatttgcgaggacgtgcctgcgggagaccc 877
                                                                                                                                           221 GECGECECECECECAAGACAAAAAAACGEGEAGCEAAGGECATGEGECAGAGGGCTG 162
                                                                                                                                                                                             ggogggtcgoctcgtcaatcctaccgctgcgtttgccatcgacatatccggtcccgcatt 937
                                                                                                                                                                                                                                       161 GGCGCACCGCGCGCCCCATCCGCACTCGAGCCGTCGCCATGGCCGCCATCATAGCTCAGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 49272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5773267.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WILLIAN R. JACOBS AND GRAHAM F. HAIFULL
TITLE OF INFORTION: D29 SHUTTLE PHASMIDS AND USES THEREOF
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADUTER READABLE FORM:
MEDIUM TIPE: 3.5 INCH 1.44 MD STORAGE
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Pred. No.
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                                                                                                                                                                                                                                                                                         ctcggctacgacaatacccccggtacc 964
                                                                                                                                                                                                                                                                                                                        CTCCACTGCCTCAGGGGCCTCGACAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                           pplication US/08614770A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SETH A. BOGOSIAN NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGANISM: MTCOBACTERIOPRAGE NDIVIDUAL ISOLATE: D29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 49.7%;
Matches 79; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: MARCH 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE CHARACTERISTIC
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RY: U.S.A.
10016
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1331 tggacccccggccggcccgaagagttagacgaagagtgcgtttttttatccgtaacgcccg 1390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSDY GLISK
COMPUTER: IBM FC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                               SOPTWARE: Patentin Release #1.0, Version #1.30
CORRENT APPLICATION DATE
APPLICATION NUMBER: PCT/DS95/09145A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.1%; Score 30.8; D
Best Local Similarity 49.4%; Pred. No. 6.1;
Matches 80; Conservative 0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Torczynski, Richard M. APPLICANT: Bollon-Tarthur P. TITLE OF INVENTION: LunglCancer Marker NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. SIDLEY & AUSTIN
1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-95
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Patent No. 5773579
                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: JOAN A HEATE
REGISTRATION NUMBER: 37,345
REFERENCE/DOCKET NUMBER: B1
TELECOMMULICATION INFORMATION
TELECHOORE: 244-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS ADDRESS STOLEY &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                      OPERATING SYSTEM
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dallas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 1.1%; Score 30.8; DB 2; Length 813; Best Local Similarity 49.4%; Pred. No. 6.1; Matches 80; Conservative 0; Mismatches 82; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1451 tatcotacttgagctgggagccttcagcaggcccggtatcaa 1492
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Torczynski, Richard M.
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Ling Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        SEE: SIDLEY & AUSTIN
: 1201 Elm Street, Suite 4500
Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application PC/TUS9509145A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/776,088
FILING DATE: 19-JUL-95
CLASSIFICATION: 435
Sequence 12, Application US/08776088 Patent No. 5773579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: EUGENIA S. Hansen
RECISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 103
ILECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         ZIP: 75270-219/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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75270-2197
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                                                                                                                                                                           Score 30.8: D
Pred. No. 6.2;
O. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung Cancer Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14. Application PC/TUS9509145A GENERAL INFORMATION:
                                                                                                                                                                         Query Match
Best Local Similarity 49.4%;
Matches 80; Conservative
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NAME: John A. Harre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JIER READABLE FORM:
SIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER
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Leica
                                                                                     CDS
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        RANDEDNESS
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                                 TOPOLOGY: 11
MOLECULE TYPE:
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PCT-US95-09145A-14
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US-08-776-088-14
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1331 tggacccccggcccccgaagagttagacgaagactgcgttttatccgtaacgcccg 1390
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                                                                                                                                                                                                                                                                               306 TGAGCACACGTCAGCGGACAGCACTTCGCCGGACGTGCACATTGTCCATTATAACTC 365
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                                                                                                       DB 6: Length 822:
                                                                                                                                                             82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1451 tatoctacttgagctgggagccttcagcaggcccggtatcaa 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 TGITCICALIGAGAIGGGCICCTICAAICCGICCIAIGACAA 467
                                                                                                                                                             0; Mismatches
                                                                                                       Score 30.8;
Pred. No. 6
                                                                                                                                                             Conservative
                                                                                                       Query Match
Best Local Similarity
Matches 80; Conserva
; CT-US95-09145A-14
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Searched: .

Run on:

Database :

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red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                          May 17, 2000, 04:26:14 : Search time 944.91 Seconds (without alignments) 12572.623 Million cell updates/sec
                                                                                                                                                                                                                                      US-09-151-189-1
2931
1 cgcggacaagccttggaaga.....aaatggcgatagatattccc 2931
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                   4857316 seqs, 2026611650 residues
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                                                                                                OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 1000000
                                                                                                                                                                                                                                      Title:
Perfect score:
Seguence:
                                                                                                                                                                                                                                                                                                                                       Scoring table:
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SUMMARIES

-LPR9042, Universite P. &	33 2 98 29	ν ξί'	rce 1. 393	if-"taxon:80365"	/clone_lib="b.drgitata sporophyte Lambda zapii /de=_stape="sporophyte" /lah host="scrip"		au, was oligo-(dr)	into a Uni-ZAPTM , CA, USA) using t	orn 83 a 127 c 107 g	ORIGIN	y Match 2.7%; Score 80.4	Best Local Similarity 55.7%, Pred. No. 68-13; Marches 215; Conservative 0; Mismatches 166; Indels 5; Gaps 3;	Oy 1035 coettatgeagtatggeacegaegaaattaceactegeggeagceaectegetgga 1094	DD 13 CCCTTCGGGAGTTCGCCAAGAACGACTACGTCAGGCTCGCCGCACAACAACCACGGC 72	Oy 1095 atgggaggetteceaaatetggaegeegtgtegataggteegatggtaeggtggaeeeg 1154	Db 73 CTGCCGGCGTTCAAGGACTCAACATTCCCGGAGCGAGGGAGGAAAGATCGACCT 129	155 ttctcccagctcttccgagcgaccttcgttggtgttgaaacggggcctttgtctctcag	130 GTCACTGATCTGTTCCGAACGACCTGGCCGGGTGTGACCACGGGTCCCGTCGTCTCTCAG	Oy 1215 ctgotcgtgaacagottcaccatcgacgctattacggtcgaaccgaagcaggagacattc 1274  D	1275 occessations tatatatates titles constitues attended attended at the constitues of the constitue of th	249 ACCCAGGGGGGGACTACAGACGCCTTCCAGCGGGGGCGACGACGACGAACGG-GGC	1335 ccccggccggccggagagagtagacgagagctgcgttttatccgtaacgcccgcgac	Db . 308 TICCAAGCIIGAAACIACITICGACGAGGAGAACCCCGCIICAICGGCAACGGCCGAGAC 367	Oy 1395 ctggccagggtctccttcgtggacaa 1420	Db 368 CTGGCCACTATTGCCTTTAGGGATAA 393	RESULT 2	925 by DNA GSS 03-JUI	prosopring meranogaster yenome survey sequence into or BACR19D16 of RPCI:98 library from Drosophila melanogaster	fly), genomi ALO53013	VERSION ALOSOLIS I GI:4934461 KETWORDS GSS. SOTTERE FILLE FILE	M Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; He	Freigotea, Neopreta, Endopretagota, Articata, Eracinotera, Muscomorpha, Ephphotota, Drosophiliae, Drosophila.	Genoscope Direct Submission	JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
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No. Score Match Length DB ID Description	80.4 2.7 393 81 AW400475 AW400475	21.0 1.0 943 04 UNSUGSIP 40.4 1.4 942 82 CNSO04NS 38.2 1.3 38.2 21 76.7798	38 1.3 324 32 AA365809 AA36580	37.2 1.3 504 28 AAG2675 AAG2675 ZGL/61	37.2 1.3 734 84 ALS14531 ARS14 36.8 1.3 468 79 ARS84526 ARS84 36.8 1.3 10A.4 83 70501509 ART10R	1. 36.4 1.2 533 26 W65709 W657	36.2 1.2 327 36 C72420	36 1.2 446 80 AW323625 AW323628	36 1.2 600 27 W84020 W84020 M84020 M8	35.8 1.2 787 82 CNSOIDB7 AL098449	35.6 1.2 446 25 D83844 D83844 D83844 B83844	22 35.6 1.2 1069 83 CNSO15BE 23 35.6 1.2 1101 82 CNSO0LdC 24 35 4 1.2 401 42 CNSO0LdC	35.4 1.2 645 82 CMSG12T3 AL1015891 35.4 1.2 645 82 CMSG12T3 AL1015891 35.7 1 2 479 30 30 30 30 30 30 30 30 30 30 30 30 30	35.2 1.2 987 9.2 CMSOUTS AMSOUTS 35.2 1.2 987 9.2 CMSOUTS 35. 3.2 46.9 70 AMJ/4804.4 AMJ	29 35 1.2 1101 82 CNSOOLXJ 30 34.8 1.2 247 80 AN407869 ANA07869	34.8 1.2 351 32 AA55352 AA35352 34.6 1.2 549 103 AA157443 AA157443	33 34.6 1.2 552 74 AV388992 AV388 34 34.6 1.2 945 82 CNSO076K AL066	34.4 1.2 592 80 C99982 C9 C99982 C9 34.4 1.2 720 49 AL632354 AL632354 AL632354	34.4 1.2 939 82 CNSOCNG ALC48395 34.4 1.2 939 82 CNSOCNG ALC59400 34.4 1.2 939 82 CNSOCNG ALC59400 34.4 1.2 1104 82 CNSOCNG ALC59400 34.4 1.2 3	40 34.2 1.2 343 24 02510 M22510 41 34.2 1.2 384 60 AI800988 AR800	AA01668 AA311661 AA311661 C	44 34.2 1.2 482 79 ANZ45544	ALIGNABAIS		RESULT. 1 And 00475	Aw400475 393 bp mRNA EST ( ON LamdiSest169est L.digitata sporophyte Lambda ZapTI		, :	Laminaria digitata		AUTHORS Crepineau, F., Roscoe, T., Kaas, R., Kloareg, B. and Boyen, C. TILE Characterisation of complementary DNAs from the Expressed Sequence		COMMENT On Dec 20, 1995 this sequence version replaced gi:1134111.  Contact: Boyen 5	Centre d'Etudes Oceanologique et de Biologie Marine

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"Web: www.genoscope.cns.fr."

"Web: www.genoscope.cns.fr."

"Web: www.genoscope.cns.fr."

"The Machination of this BAC-and sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDCP). The Machination with the Barkeley Drosophila Genome Project (BDCP). The Machination of this BAC-and the Drosophila melanogaster genome using the AGE-s for further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC ilbrary was prepared by Kazuroty Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Aaron Mammoser in Pieter de Jong's laboratory in the Department of NY. The library is named ReCI-99 and was constructed by partial EcoRI digestion of Drosophila DRA provided by the BDCP-from the isogenic strain y? on bw sp. the same strain used for the BDCP's Pl and EST libraries. A more detailed description of the library and how to order individual RAC clones, the entire library, or filters for hybridization from the BACPAC Resource.Center can be found at http://bacpac.med.lufalo.edu/drosophila_bac.htm.

"In 942 "In 942" "In 944" "In 
                                                                                                                                                                                      Direct Submission
Submitted (02-JUN-1999) Genoscope . Centre National de Sequencage :
BP 191 91006 EVRx cedex - FRANCE (E-mall : seqréfégenoscope.cns.fr
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DEFINITION 1999911 r1 Stratagene lung (#937210) Homo sapiens CDNA CLONE IMAGS:79956 5 similar to 95:021260 CLATHRIN HRAY CHAIN (HURAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2675 caggacgtatatetetggtageggtetgttaagaa,etteeacaagaeegttaegtttgg 2734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2795 ggtgtaagacatattttttctcctgttatggatctgtagaacagctaggtgttgttttata 2854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2615 giggcagigtamacmamagaggatgiagictcgccctcagiilggagagiacgiaggigg 2674
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1. (Dases 1 to 382)
                           Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases I to 942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 35milarity 25.6%; Pred. No. 0.92; Length 942; Similarity 25.6%; Pred. No. 0.92; j. j. foots of 65; Conservative 65; Mismatches 127; Indels 0
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/clone_lib-*RPCI-98
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/note-'end : T7*
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ORIGIN
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T62798
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                                                  - Wab: www.genoscope.cns.frace.compare representations.compare the collaboration of this BAC-end sequence was/carried out as part of a collaboration with the Backedey Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fultily.org the BDCP Drosophila melanogaster BAC library was prepared by Kazucyo Osoegawa and Aaron Mammoser in Pieter de Jong is laboratory in the Department of Cancer Genetics at the Roswell park Cancer Institute in Buffalo. NT. The library is named ReC198 and was constructed by partial Ecost digestion of Drosophils DNA provided by the BDGP from the 190genic strain ys; on by sp, the same strain used for the BDGP's pl and EST libraries A more detailed description of the library and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library found at http://bacpac.med.uffalo.edu/drosophila_bac.htm.
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Wab : www.qenoscope.cns.fr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit fly.
Drosophia melanogaster
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS004NS 942 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR10M21 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 t 511 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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VERSION
KEYWORDS
SOURCE
ORGANISM
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CNS004NS/c
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E (bases 1 to 324)

S Adams, M.D. Keriavage, A.R., Frischmann, R.D., Fuldher, R.A.,

Bull, C.J. Lee, N. H. Kirkess, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Ciling, T.R., Cotton, M.D., Barle Hughes, J., Fine, I.D.,

Fitgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gheim, C.L., Hanna, M.C., Hedblom, E., Hinke, P. S.J.,

Keiley, J. M., Keiley, J., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriey, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y.,

Bodnarik, D.P., Greene, J.M., Gruber, J., Hudson, P.F., Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Walson, P.F., Kim, A.K.,

Kaymond, L., Wei, Y.F., Wingjun, J., Li, H., Walssner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wingjun, J., Li, H., Walssner, P.S., Olsen, H.,

Bullion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fleids, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: Mi3 Reverse.
Location/qualifiers
1. 324 %
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 CIGATITITAAAIGAGGGTAAAAGGCCCICTAACCIAIGCAGGTITCCCCATIAIGCAIA 205
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     Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Mammaiia:
Eutheria; Primates; Catarrhini; Rominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: pineal body; Vector: pBluescript SK-;
Ste_1: EcoRI; Stte_2: Xho!"
STO C 62 9 90 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1995 this sequence version replaced gi:637866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockviile, MD 20850 USA
Tel: 3018699056
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/db_xref="ATCC (inhost):170458"
/db_xref="taxon:9606"
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/dev_stage* adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlavetigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High qailty sequence stops: 302 Source: IMAGE Consortium, LINL This cione is available royalty-free through LiNL; contact the IMAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 499 Std Error: 0.00
Billier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Bultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Hawkins, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Scares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 TAGAAAATGCTAGTATGTTTTGCTCACTTCATATGTAACAGGTGCCCTTATGTTGTGCTG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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5' end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington Diversity School of Medicine.
4444 Forest Perk Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Enail: estlekatson.wustl.edu
Insert Size: 499
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similar to clathrin, heavy polypeptide, mRNA sequence.
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close IMAGE:512875 3' similar to gb:D21260 CLATHRIN HEAVY CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausbergenih.gov
Tissue Procurement: DCTD_ATTP CDNA Library Preparation: Ling
Tissue Procurement: DCTD_ATTP CDNA Library Preparation: Ling
Tissue Procurement: DCTD_ATTP CDNA Library Arrayed by: The I.M.A.G.E.
Rossortium (Lilli) DNA Sequeacing by: Berkeley MGC sequencing
project clone distribution: MGC close distribution information can
be found through the I.M.A.G.E. CONSORTIUM_TISS.
WWW-bio.lin.igov/DETP_IMAGe_Atmage hitml Base Calling / Quality
Scores: PHRED from University of Mashingtion Genome Center: Vector
Trimming: cross_match from University of Washingtion Genome Center:
PHRAP Suite: Poly Tidentification: patwatch.pl from Berkeley
Drosophila Genome Project. Ualversity of Washingtion Genome Center:
http://www.genome.washington.edu
plate: LLCH7 row: i. column: 6
High quality sequence stop: 369.
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/call_line="Nord"
/lab_host="DH10B (phage-resistaat)"
/lab_host="DH10B (phage-resistaat)"
/lote="Organ: lung' vector: poTB7; Site_l: XhoI; Site_2:
BCOKI; DNN ande by oligo-dr priming. Directionally
closed into EccRI/AboI sites using the following 5,
adaptor: GGCAGAG(G). Site-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Geraid M. Rubin (University of
Callfornia, Berkeley) using ZAP-CDNA systhesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
97 a 108 c 184 g 101 t
2821781.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821781 5', nRNA sequence.
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AA062675/c AA062675 504 bp mRNA EST 01-DEC-1996
LICCUS EMOLITION : EMOLITION : EMOLITION : SEMINATION : EMOLITION : SEMINATION : EMOLITION : 
                                                                                                                                                                                                                                                              Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutharia; Primates; Catarrhin1; Hominidae; Homo.
1. (bases 1 to 490)
11. (bases 1 to 499)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 gecagggteegeategetacegettiggetgtggtactggeegeacectgtttggeatte 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 ACAACCGATCCCGTGGGTACCGTGGTGGCTCCGGGGGCCGGGGGCTTCTTCCGTGGGG 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hed (1999 s):
1999 this sequence version replaced gi:5408858.
Ts: 1891781.3prime
Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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/clone_11b="WIH MGC_7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
                                                                                          AW250569
AW250569.1 GI:6593562
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DEFINITION
                                                                                                                                                                                                                                                                         ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
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                                                                                               AGCESSION
                                                                                                                                                                                    KEYWORDS
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Hiller, L. Leason, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiacof, G., Becker, M., Bonauder, Favello, A., Gish, W., Bankias, M., Hillman, M., Kuceba, T., Lacy, M., Le, M., Le, M., Mandis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikin, E., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwyood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 607-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2402 accatgiacattggattgcagiaagigcggttagagagggatacgitaaacgigcitgcc 2461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2462 igigiataigatacatitgicaiggaaataitagaatgegtigactigacticaceatga 2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2522 aataccatgatcgcgtggtgtgctgctttcacctgtcggagcggtacgtaagatgtgctt 2581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 AGATCGTACACTGGATTGCAGTGCTTCCCAGATTATTGAAANATGTTACAGACAACTTGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 CIGATITITAAAIGAGCGTAAAAGGCCCTCTAACCTAIGCAGGITICCCCAITAIGCAIA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Etheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2582 tctactgagcogtttgtgtttagtccattccgcgtggcagtgtaaacaaagaggat 2637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cloae="IMAGE:512875"
/cloae_11b="Stratagese corneal stroma (#937222)"
/dev_stage="76 years"
/deb_host="80LR cells (kahamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                  On Nov 29, 1993 this sequence version replaced gi:637708 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 37.2: .DB 28; Length 504: 47.0%; Pred. No. 5.7; tive 0; Mismatches 125; Indels 0;
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/organism="Sorghum bicolor"
/db_ref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; vector: Lambda Zap; Site_l: XhoI; Site_2:
ECORI: The library was made from poly-A RNA in the cloning
vector lambda_ZAP II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum bicolor
Bukaryota, Mildiplantae, Streptophyta; Embryophyta: Tracheophyta:
Bukaryota; Viridiplantae, Streptophyta; Embryophyta: Infopsida; Poales:
Poaceae: Sorghum
1 (bases 1 to 468)
Cordonnier-Pratt, M. M., Gingle, A., Fratt, L. and Paterson, A.
Di Ext attabae from Sorghum
On bulished (1999)
On Jul 7, 1999 this sequence version replaced gi:5406972.
Contact: Cordonier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmprattegg.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
                                                                                                                                                                                                                                AW284526 468 bp mRNA EST 03-FEB-2000
IG1_270_C03.91_A002 Light Grown 1 (IG1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSO15OE 1044 bp DNA GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN14C06 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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1.3%; Score 36.8; DB 79; Length 468;
Best Local Similarity 50.6%; Pred. No. 7.2;
Matches 89; Conservative 0; Mismatches 87; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Botany
The University of Georgia
The University of Georgia
But Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1805
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start...64
High quality sequence stop: 468
POLYA-res.
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ORIGIN
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa: Chordata; Cranlata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 752)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Rucaba, T., Lacy, M., Leh, M., Martih, J., Morris, M.,
Schallenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Sosres, B., Wilson, R. and
                                           #1314531 752 bp mRNA EST 17-DF0-1998
UJ48602.y1 Sugabo mouse liver mits Aus musculus CDNA clone
IMAGE:1923147 5: similar to gb:D78135 Mouse mRNA for CIRP (MOUSE);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed by Dr. Sumio Sugments <1.5kb. Library constructed by Dr. Sumio Sugmon (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGGG and 3' end primer CGACTGCAGCACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zmail: mouseest@watson.wustl.edu
Ins clone is available royalty-free through LLNL : contact the
TMAGS CORSOTLUM (infedimege.llh.gov) for further information.
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Uppublished (1996)
On Jan 19, 1998 this sequence version replaced g1:2045628.
Contact: Marra M/Mouse EST Project
WashD-HMI Mouse EST Project
WashIngton University School of Medicinep
444 Forest Park May, Box 8501, St. Louis, MO 63108
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/clone="iMAGE:1923147"
/clone=lib="sugano mouse liver mlia".
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                                  752 bp
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Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:1255037"
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Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                          Submitted (23-701-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRV cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project grant. The DNA was prepared from embryos by Alain Bucheton and Generieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .W45709 533 bp mRNA EST 22-MAY-1996 zc27d03.s1 Soares_senectent_flbroblasts_NDHSF Romo sapiens cDNA clone_IMAGE:323525 3', mRNA sequence.
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Bukaryota Metazoa: Chordata: Craniata; Vertabrata; Mammalia: Eutharia; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 533)
14 (lark, N. Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Rultman, M., Rucaba, T., Le, M., Esnnon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmana, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                           fruit fly
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
Pterygota, Meoptera, Endopterygota; Diptera, Brachycera,
Muscomorpha: Ephydroidea, Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/plasmld="pBeloBAC11"
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Pred. No. 12;
1; Mismatches
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Contact; Wilson RK
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AL105704.1 GI:5617858
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Best Local Similarity 50.0%;
Matches 89; Conservative
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Eukaryota Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales: Poaceae; Oryza; 1 (bases 1 to 610) Wing, R.A. and Dean, R.A. who Dean, R.A. and Dean, R.A. or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /coore_INTERS 32355.
/clone_INP-%Coares senescent_fibroblasts_NDHSF.
/tissue_type=%senescent fibroblast
/tissue_type=%senescent fibroblast
/lab_host=%bH10B (ampicillin resistant)*
/note=%vector: pTT73B (Pharmacia) with a modified
/note=%vector: PTT73B (Pharmacia) with a modified
polylinker, VIYPE: phagemid; Site_1: Not I: Site_2: Eco
RI: lst strand cDNA was primed with a Not I - oligo(dT)
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DEALL: estGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: mob.NEGAFT
High quality sequence stop: 300.
Location/Qualifiers
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/clone_lib="Rice panicle at flowering stage"
/dev_stage="flowering stage"
/note="Organ: panicle; Rice cDNA from panicle at flowering stage"
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                    On Sep 12, 1996 this sequence version replaced gi:1402260.
Contact: Takuli Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
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Best Local Similarity 52.7%; Pred. No. 8.8;
Matches 77; Conservative 0; Mismatches 69; Indels 0
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/strain="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4530"
/clone="E1585_1A"
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Location/Oualifiers
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                                                                                                                                                                                                  Tel: 0298-38-7441
Fax: 0298-38-7468
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                                                                                                                                                                                                                                                                                                                                                                                                                     candidate in its interest their primary source of carbohydrate. Monocytedonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arnunganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare: variety. The library contains 30, 864 clones with an average lasert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 % Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening.*
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                                                                                                                                                                                                                                                                                                                           /note-"Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world Half of the world population especially those inhabiting highly populated areas of the humid tropics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  975 totoctgagotogocgotoagttggoggagotatactggatggogctggocagggatgta 1034
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                                                                                                                                                                                               /db_xref="taxon:4530"
/clone="hbxb0089L05r"
/clone=11b="crg1 Rice BAC Library"
/tissue_type="teaf"
/lab_host="E.coll DR108"
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Sasaki, T. and Yamamoto, K.
Rice cDNA from panicie at flowering stage
                                                                                                                   /organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
                                                 Bigh quality sequence stop: 360.
Location/Qualifiers
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 bp
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Oryza sativa
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KEYWORDS
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CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Dish Sequencing by: Washington University Genome Sequencing Content of Marithution: NGT-CGAP clone distribution information can be found through the I.M.G.E. Consortium/Libri at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fissue Procurement: Lee Reiman, M.D., Michael R. Emmert-Buck, M.D.,
                                                                                                                                                                                                                                                                                                                                                                      AA491660 334 Mb mrna EST 19-AUG-1997.
ne79902.si NCI_CGAP_Evi Homo sapiens cDNA clone IMAGE:910514, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dukaryota; Metazoa; Chordata; Craniata: Vertebrata; Mammalia; Bukaryota; Metazoa; Catarrhibi; Hominidae; Homo.

1. (bases 1 to 334)

NCI-CGAP http://www.ncbl.nim.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
123 GAGGIACGCGCCGCTCACCACNTCGCACGCCTCGTCGTCGTCGACGCTCGCCACCTCGGT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397827.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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May 17, 2000,
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Job time: 2905 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI CGAP http://www.ncbl.nim.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 TCTTCTCCCCACCCGGGGTATGAAGAATTCATCAGCACTGAACTTATAAAGCCATTCATC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 CARAAAGTGAAACAGAAGAGACTGTAAGTCATCTCCTTGGGTTTCTACTTCTACTGTTTG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          karyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 446)
                                                                                                                                                                                                                Sizc-selected on agarose gel, average insert siz
Reference: Krizman et al. (1996) Cancer Research
[5.380-538].
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                                                                                                                                                                                                                                                                                                                                                Score 36; DB 34; Length 334;
Pred. No. 10;
0; Mismatches 86; Indels
                                                                                                                                                                     r: pampl0; mRNA made
oligo-dT priming. N
ET from Amersham
                                                                                           /clone_inage:910514"
/clone_lib="NCI_CGAP_EW1"
/tissue_type="Ewing's sarcoma"
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                                                                                                                                                                                                                                                                        109 t
                                                        /organism="Nomo sapiens"
/db_xref="taxon:9606"
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/strain="FVB/N"
/db_xref="taxon:10090"
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High quality sequence stop: 4
Location/Qualifiers
                 Location/Qualifiers
1. .334
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-40m13
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CDNA Library
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Matches 87; Conserve
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  Sed primer:
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Email: P
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AW323625
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                    FEATURES
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/note-"organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned undirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH*

1 106 c 164 g 87 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 agggteegeategetaeegeffttggetgtggtaetggeegeaeeetgtttggeattegae 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 ACCGGTCCCGAGGATACCGGGGTGGCTCTGCTGGAGGCCGGGGGCTTTTTCCGTGGGGGAC 362
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                         DB 80; Length 446;
                                                                                                                                                                                                                                                                                                                   Score 36; DB 80; Length 44
Pred. No. 12;
0; Mismatches ·85; Indels
samble
e-"tumor, biopsy a
                                                                                                                                                                                                                                                                                                                       1.2%;
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.6
Matches 87; Conservative
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Thu May 18 22:21:28 2000

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L35496 Clostridium botulinu X81714 C.botulinum bont/f 9 1 U67490 Methanococcus janna i AE001898 Deinococcus radio
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/codon_start=1
/codon_start=1
/product="vanadlum bromoperoxidase"
/protein_id=*Add35279.1*
/db_xref="G1:3582763"
/translation="MLCHAADTTRGSPMPDTGVLRLLISSORAKGWRRQLEGEKSLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FITDAITVEPROETFAPDINTHVDFPEFALNIONGGPAGPEELDEELRFIRNANDLAN
VSFVDINTREATROSLILELGAFSROGINGFIDSDROGGVNECTRIGAB
LAQRASCYGKWONTRARPEALGGTLHNT RADILAMEDISLENDELLKRVAETRAA
QURNNERTYLLPQAIOVGSPHIPSTSGRAVONGAFATVIKALIGIDAGGEGFRPYF
PSDGGLEILNFGAGGTLYTEGGENKLAVNVAFGRONIGHTHREDGIGGLLGETITVRT
LIQGILATPAEEATFERLFTGENKLAVNVAFGRONIGHTHREDGIGGLLGETITVRT
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EVTASGYPPEHKHTGEGRHLGTCINSDALDAPARNROVAFASRARBENGG
GIVCOLTINGETDAFFRERSLEDELLOPADDFALEDCILNGDESICEDVPAGDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-MAR-1998) Environmental Science, Policy and Management, University of California, 201 Wellman Hall, Berkeley, CA 94720-3112, USA
                                                                                                                                                                    AF053411 2931.bp mRNA PLN 12-SEP-1998
Fucus distichus vanadium bromoperoxidase mRNA, complete cds.
AF053411
                                                                                                                                                                                                                                                                                      Fucus distichus
Fucus distichus
Fucus distichus
Eukaryota; stamaenopiles; Phaeophyceae/Xanthophyceae group;
Phaeophyceae; Fucales; Fucaceae; Fucus
1 (Asss 1 to 2931)
Vreeland, V., Wg. X. and Epstein, L.
Direct Submission
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Ratio: 5.246 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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/db_xref="taxon:3012"
/dev_ztage="2-cell embryo"
1. .227
              145.70
146.13
487.56
560.23
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            118.80
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                                                                                                                    seq_name: gb_pl2:AF053411
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LOCUS AF053411
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            9b_bal:CLOBONT
9b_bal:CBBONTFG
9b_ba2:U67490
9b_ba2:AE001898
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6055 1.AF044733 Trypanosoma cruzi cic
6055 1.AF044732 Trypanosoma cruzi cic
103576 1.AE001098 Arabidopsis thalian
15513 1.AE001696 Tharbidopsis thalian
1527 1.X71415 Artographa californica
909 1.AE00134 Prorocentrum micans mi
926 1.AF034395 Uncultured markine bact
1323 1.AE00133 Prorocentrum micans mi
26263 1.AF074946 Hemorrhagic enterity
934 1.X1123 D.Biseptata mRNA for var
6583 1.AE0048 R.EYPINOPOLIS DNA, 205
133894 1.AE010545 Sequence 1 from Pater
133894 1.AE010545 Homorranas chrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2035 1 AFUDJALL KUCUB DIBLILIGER ME
1794 1 E1720 Corallina pilulifera mF
1791 1 E1720 Corallina pilulifera mF
2029 1 D87658 Corallina pilulifera mF
12198 1 AE001953 Delnococcus radiodus
2034 0 1 AL022076 Mycobacterium tuberd
2103 1 Ull272 frypanosoma cruzi clone
2013 1 U06070 Irypanosoma cruzi tulah
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| 282005 R.erythropolis DNA, 205
| AC023415 Homo saplens chromos
| 106829 Mouse cytomegalovirus
| AR031631 Sequence | Ifrom pater
| AR031631 Sequence | Ifrom pater
| AR031631 Sequence | Ifrom pater
| In19784 Secherichia coli MS@ac a
| S76749 toxin [Clostridium botu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4704 V00741 MOUSE MRNA encoding the 4749 J00380 mouse epidermal growth 4750 I 108331 Sequence I from Patent 108380 I AC012251 Homo sapiens clone 1830 | X85369 C inaequalis mRNA for v
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1 AF038023 Herpetomonas roitman
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-O-Y-COPA2_1/12PTO_spool_/VSOS151189/runat_15052000_082513_1608/app_query.fasta.1
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-OB-Genbbl -OFMT-fastap -SUFFIX-41-676_rage -GAF0P-12_000
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-DELCOP-6.000 -FGAPEXT-7.000 -YGAPEXT-0.500
-DELCOPC-0.000 -FGAPEXT-7.000 -YGAPEXT-0.500
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-MANTALN-1000000 -USER-GCOALIGN-200 -TMR_SCORE-pct
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            out_format : pfs
                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
of: US-09-151-189-2_COPY_441_676 to: GenEmbl:*
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Oucry: US-09-151-189-2_COPY_441_676
Oucry: Usryth: 236
Database: GenEmbl:*
Database sequences: 882769
Database length: -486395729
Search time (sec): 483.650000
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9b_htg2:HSA324122
gb_ba2:ECU19784
9b_ba1:S76749
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b_pl1:p87657
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dovfevdrdedklvkssfkgtlfvagelakladniaigrmmagvhyfsdoffsllige
bromoperoxidase from a marine macro-alga, Corallina pliulifera
FEBS Lett. 428 (1-2), 103-110 (1998)
98307393

    MCIPADNLOSRAKASFDIRVAAAELALNRGVVPSFANG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 rValLeuLysAlaLeuIleGlyLeuAspArgGlyGlyGluCysPheProA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HisTyrPheArgLeuile ... GlyAlaAlaGluLeuAlaGlnArgAlaSe 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 rCysTyrGlnLysTrpGlnValHisArgPheAlaArgProGluAlaLeuG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 snGluvalThrTyrLeuLeuProGlnAlaileGlnValGlySerProThr 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 ASPALAASPPheASPIleSerLeuLeuGluAsnAspGluLeuLeuLysAr
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Percent Identity: 38.393
                                                                                                                            /organism="Corallina pilulifera"
/db_xref="taxon:78447"
/clone="BPO1"
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Department of Pharmacology; Pujishiro-dai 5-7-1, Suita, Osaka 565,
Japen (E-mail:tanabeerl:ncvc.go:jp, rel:06-833-5012,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D87657 2035 bp mRNA PLN 07-JUL-1998
Corallina pliulifera mRNA for vanadium-dependent bromopèroxidase 1,
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Shimonishi, M., Muwamoto, S., Inoue, H., Wever, R., Ohshiro, T.,
Igumi, Y. and Tanabe, T.
Cloning and expression of the gene for a vanadium-dependent
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Corallina pilulifera
Corallina pilulifera
Corallina pilulifera
Eukaryota: Rhodophyta: Florideophyceae; Corallinales;
Corallinaceae; Corallinoideae; Corallina.

[ pases 1 to 2035)
                                                                                                                                                                                                                                                                                                 1948 TAATCAACTTCGAAGGGGCATGCCTTACATGAGGGAGAGATCAACAG 1997
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                                                 1698 ICCCITCTIGAAAIGAIGAGCICTIGAAACGIGIGGCGGAGAIAAAIGC 1747
                                                                                                                                                   1748 GGCGCAGAATCCCAACAACGAGGTCACCTACCTTCTTCCACAAGCTATCC 1797
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           67
                                                                                                        8
                                                                                                  67 aAlaGlnAsnProAsnAsnGluValThrTyrLeuLeuProGlnAlalleG
51 SerLeuLeuGluAsnAspGluLeuLysArgValnlaGluIleAsnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gPheAspGlylleGlnGlyLeuLeuLeuGlyGluThrIleThrValArgT
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1576 TICAAGGGAACT. CTCACTGTTGCCGGTGAATTGAACAAGCTCGCCGA 1622
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                                                                                                                                                                                                                                                                                                                                                                                                     1388 CIGAICCIICAIICCIGIIGCCGAIGGCAIICGCCGAGGCCAGCCCAIIC 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1438 CATCCGTCCTACGGAAGCGGCCACGCTGTGGTGCTGCCGCCATGTGTGAC 1487
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                                                         1188 ACGUACCAGAAGTTTAACATTCATCGTCGCCTGCGCCCTGAGGCTACCG 1237
                                                                                                                                         1238 GIGGICIGATTATCGITAACAAATCGCACCGCAGAAGGGCCAGAGCAIT 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                             90 HisProSerTyrProSerGly#IsAlaThrGlnAsnGlyAlaPheAlaTh 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 PheGluGlyAlaCysLeuThrTyrGluGlyGluIleAsnLysLeuAlaVa 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153. lasnvalalapheGlyArgGlnMetLeuGlyIleHisTyrArgPheAspG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 lylleGinGlyLeuLeuLeuGlyGluThrIleThrValArgThrLeuHis 186
                                                                                                                                                                                                                                                                      61 gvalalaGluileAsnAlaGlnAsn......ProAsnA 73
                                                                                                                                                                                                                                                                                                                                                           73 snGluValThrTyrLeuLeuProGlnAlaileGlnValGlySerProThr 89
                 E
                                                                                                                                                                                      45 AspAlaAspPheAspIleSerLeuLeuGluAsnAspGluLeuLysAr
              16 rCysTyrGlnLysTrpGlnValHisArgPhcAlaArgProGluAlaLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lzumi V. and Tanabe, T.
Ngw HALOPEROXIDASE GENE AND IIS UTILIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-1997 JP 1997070539
                                                                                                 33 lyGly...ThrLeuHisAsoThrIleAla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1773 TGATGGAACTACAATCCAGATC 1794
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JP 1998248581-A/2.
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KNIS/09,C12N9/08,(C12N15/09,C12R1:89),(C12N9/08,C12R1:19);
andedness: Double;
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/organism='Corallina pilulifera' FT
                                       1703 TTCAAGGGAAGT...CTCACTGTTGGCGGTGAATTGAACAAGCTCGCCGA 1749
                                                                                                                       1850 GAGCAAAGTCTCACGTAIGGCGAAGIICIICIICIICAACIIGCCGAAGII 1899
                                                                                                                                                                                                                           1800 AGITCGAGTCACTTCTGCTCGGTGAGCAGGTTGCGATTGGAA 1849
137 PheGluGlyAlaCysLeuThrTyrGluGlyGluTleAsnLysLeuAlaVa 153
                                                                                                                                                                                 170 lylleGinGlyLeuLeuLeuGlyGluThrileThrValArgThrLeuBis 186
                                                                                                                                                                                                                                                                   187 GlnGluLeuMetThrPheAlaGluGluAlaThrPheGluPheArgLeuPh 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1138 CACCTGTGAGTCTGGTGACTGAAGTGGCTACGCGCGCGTGAAGGCGGT 118
                                                                                            153 lAsnValAlaPheGlyArgGlnMetLeuGlyIleHisTyrargPheAspG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HisTyrPheArgLeuile...GlyAlaAlaGluLeuAlaGlnArgAlaSe 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product='holoperoxldase'
Location/Quallflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA PAT
mRNA for haloperoxidase.
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Gaps: 8
Percent Identity: 38.393
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/organism="unidentified"
/db_xref="taxon:32644"
. 481 c 505 g 41:
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OS-09-151-189-2_COPY_441_676 x E17199
                                                                                                                                                                                                                                                                                                                                                                                                   1900 IGAIGGAACIACAAICCAGAIC. 1921
                                                                                                                                                                                                                                                                                                                                                        203 eThrGlyGluValTleLysLeu 210
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mat_peptide
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1998248581-A/1.
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2.276
63.839
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LOCUS E17199
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Ratio:
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ORIGIN
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AUTHORS
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Submitted (02-SEP-1996) to the DDBJ/EMBL/GenBank databasea. Tadashi
Tanabe, National Cardlowascular Center Research Institute,
Department of Pharmacology; Fujishiro-dai 5-7-1, Suita, Osaka 365,
Japon (E-mail:tanabedil:cvc.go.jp, Tel:06-833-5012,
                                                                                                                                                                                                                                                                                                    D87658 2029 bp mRNA PLN 07-JUL-1998
Corallina pilulifera mRNA for vanadium-dependent bromoperoxidase 2,
complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELYLMALGRDIEFSEFESPKNAAFIRSAIERLNGLEWFNTPAKLGDPPAEIRRRRGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2029)
Shinodishlik, Kuwamoto,S., Inoue,H., Wever,R., Obshiro,T.,
Isumi,Y. and Tanabe,T.
Cloning and expression of the gene for a vanadium-dependent
bromoperoxidase from a marine macro-aiga, Corallina pilulifera
98307393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vanadium-dependent bromoperoxidase 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Rhodophyra, Florideophyceae, Corallinales,
Corallinaceae, Corallinoideae, Corallina.
                                                1649 GIGITCACIACITCTCTGACCAGTICGAGTCACIGCTACTCGGTGAACAG 1698
                                                                                                                                 1699 ATTGCGATTGGAATCTTGGAGGAGCAGACCTGACGTATGGCGAGAACTT 1748
163 lylleHisTyrArgPheAspGlylleGinGlyLeuLeuLeuGiyGluThr 179
                                                                                          180 IleThrValArgThrLeuRiaGlnGluLeuMetThrPheAlaGluGluAl 196
                                                                                                                                                                                                                                                                                                                                                                                                      D87658.1 GI:3293051
varadium-dependent bromoperoxidase 2.
Corallina pilulifera CDNA to mRNA, clone:BPO2.
Corallina pilulifera
                                                                                                                                                                                                        1749 CTICTTCAATTTGCCGAAATTCGACGAACTACAATCCAGATT 1791
                                                                                                                                                                          196 aThrPheGiuPheArgLeuPheThrGlyGluValIleLysLeu 210
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    2029
    /organism="Corallina pllulifera"
/db_xref="taxon:78447"
    /alone="BPO2"

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US-09:151-189-2_COPY_441_676 x D87658
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FEATORES
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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
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         .IUMI YOSHIKAZU, TANABE TADASHI
:12N15/09,C12N9/08,(C12N15/09,C12R1:89),(C12N9/08,C12R1:19);
                                                                                                                                 1. .1791
/organism='Corallina pilulifera' FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1182 ACGGTATCAGAAGTTTAACATTGATCGTCGCCTGCGGCCTGAGGCTACTG 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1232 GIGGICIGATIATCGTTAACAAGAAATCTTTCCTTGCGGGTAGT..... 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1276 .....GATATATATTCCCTGAAGTTAGTGAAGTGGTCGAGGAGCT 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1317 CTGATCAATTGTGGATGACGTTGCTGAGGGCAATGAAAAACAGAACAGGG 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1467. TGCTGGCGCATGTGTGACATCCTCAAGGCGTTCTTCGACGCCAACTTC 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1417 GCCGAGGGCAGCCCATTCCATCGTCTATGGAAGTGGCCACGCTGTGGT 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1517 AGATCGATAAGGTGTTGGAG. ....GTCGACACTGATGAG 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1552 GACAAGCTTGTGAAGTGGTCTTTCAAGGGAACT...CTCACTGTTGCCGG 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 GlnVaiGiySerProThrHisProSerTyrProSerGlyHisAlaThrG1 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 . LeuAspargGlyGlyGluCysPheProAsnProValPheProSerAsp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 AspGlyLeuGluLeulleAsnPheGluGlyAlaCyaLeuThrTyrGluGl 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yGlulleAsnLysLeuAlaValAsnValAlaPheGlyArgGlnMetLeuG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HisTyrPheArgLeulle ... GlyAlaAlaGluLeuAlaGlnArgAlaSe 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1367 CIGACGGGATHGTGAGCCCGGATAAATCATITCTGTTGCCGATGGCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 nAsnGlyAlaPheAlaThrValLeuLysAlaLeuIleGly......
                                                                                                                                                                                                   /product-'haloperoxidaae'
1. .15191
Ab_xref="taxon:32644"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 38.095
                                                                                          Location/Oualiflers
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Gaps:
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US-09-151-189-2_COPY_441_676 x E17200
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trandedness: Double;
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Rey
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mat_peptide
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anslation="MTSSAPESSALPDVLHLGYSFCPNDTFIFHALHAGLVQGPLPVQ
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LVDTVDLRSRTSAYRFRVDDPVGAAALLERQPYVRKATPRPPYAVAQLGAQANVPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>RFTYPEYGLDKLLDLGAWWEGETGLPLPLGAILVRRDLPAQTQRELQDAVRRSLE</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ranslation-"MSKASAPAFPAVEVRGLSKSYGRANVLTDVFLNVIPGEVYALTG
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                                                                                                                                                                                                                                               Richardson, J. D. Richardson, D. L., 27, M., Shen, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    d (08-NOV-1999) The Institute for Genomic Research, 9712 Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r to GB:AE000657 percent identity: 62.08; sequence similarity; putative" .
                                                                                                                                                                                                                                            white,O., Elsen,J.A., Heldelberg,J.F., Hickey,E.K., Peterson,J.
Dodson,R.J., Raft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L.
Moffat,K.S., Qin,H., Jang,L., Pamphile,W., Crosby,M., Shen,M.,
Vamathevan,J.J., Lam,P., McDonald,L., Otterback,T., Zalewski,C.,
Makarova,K.S., Aravind,L., Dally,M.J., Minton,K.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r to GB:AL009126 percent identity: 54.74; sequence similarity; putative"
                                                                                                                          Genome sequence of the radioresistant bacterium Deinococcus
             wa.K.S., Aravind.L., Daly,M.J., Utterback,T., Zalew.
hmann,R.D., Ketchum,K.A., Nelson,K.E., Salzberg,S.,
sequence of +ks.—and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                           M.J., Minton, k.w.,
Nelson, K.E., Salzberg, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transporter, ATP-binding protein"
AF10588.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product-"conserved hypothetical protein"
protein id-"AAF10587.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note='ldentified by Glimmer2; putative'
'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism-"Deinococcus radiodurans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vyevtporfdlyeyyrerveya"
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                                                                                                                                                                                                                                                                                                                                                              on, Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"similar to GB:AL009126
                                                                                                                                             radiodurans R1
Science 286 (5444), 1571:1577 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTARPELPLFVGDAAEAGTPTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:1299"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DR1011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R1012"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /qene="DR1013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "DR1011"
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                                                                                                                                                                                                                        (bases 1 to 12198)
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                                                                                                                                                                                                                                                                                                                                                                                                                Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                  MEDLINE
REFERENCE
AUTHORS
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JOURNAL
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Rl section 90 of 229 of the complete
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Baft,D.H., Gwinn,M.L., Melson,W.C.; "Richardson, D.
                                                                                                                                                                                             1349
                                                                                                                                                                                                                                                                                   1350 GIGGICIGATIAGCGITAACAAGAATCTITCCTIGGGGGTAGT..... 1393
                                                                                                                                                                                                                                                                                                                                                                                    1434
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                                                                                         1250 CACGTGCTGAGTCTGCTGAAGTGGCTAGGCGCGCGTTGAAGGCGGT 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .... GTCCACACTGATGAG 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1767 GIGITCACIACITCICIGACCAGITCGAGICACIGCIACICGGIGAACAG 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTGGCGCATGTGTGACAATCCTCAAGGCGTTCTTCGACGCCAACTTCC 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1817 ATTGCGATTGGAATCTTGGAGGAGCAGAGCCTGACGTATGGCGAGAACTT 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGAGGCCAGCCCATTCCATCGTATGGAAGTGGCCACGCTGTGGT 1584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 .. LeuAspArgGlyGlyGluCysPheProAsnProValPheProSerAsp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lylleHisTyrArgPheAspGlylleGlnGlyLeuLeuGlyGluThr 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleThrValArgThrLeuHisGluGluLeuMetThrPheAlaGluGluAl 196
                                                                                                                                                                                                                                            45
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                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                            1 HisTyrPheArgleuile...GlyAlaAlaGluLeuAlaGluArgalaSe 16
                                                                                                                                        16 rCysTyrGlnLysTrpGlnValH1sArgPheAlaArgProGluAlaLeuG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria: Thermus/Delnococcus group; Deinococcus. 1 (bases 1 to 12198) 1 (bases 1 to 12198) 2 (battelo.). Naidelberg. TF. Niever F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1435 CTCATCAATTCTGGATGACGTTGCTGAGGAGCAATGAAAAACAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 snAsnGluVal.....ThrTyrLeuLeuProGlnAlaile
                                                                                                                                                                                       1300 AGGERICAGASGITIAACATICATGGTCGCCTGCGGCCTGAGGCTACTG
                                                                                                                                                                                                                                      lyGlyThrLeu...........HisAsnThrIlealaGlyAspLeuAsp
                                                                                                                                                                                                                                                                                                                                     46 AlaAspPheAspIleSerLeuLeuGluAsnAspGluLeuLeuLysArg...
                                                                                                                                                                                                                                                                                                                                                                                 .....GATATATATTCCCTGAAGTTAGTGAACTGGTCGAGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                 1485 CIGACGGAIIGIGAGCCCGGAIAAATCAIIICIGIIGCCGAIGGCAIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspGlyLeuGluLeulleAsnPheGluGlyAlaCysLeuThrTyrGluGl
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to: 2029
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LOCUS AE001953 12198 bp
DEFIMITIDN Delnococcus radiodurans
from: 1
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Deinococcus radiodurans
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AE001953.1 GI:6458740
to: D87658
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Align seg 1/1
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AUTHORS
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KEYWORDS
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ranslation-"MTQGSVVDPRPAQVRAALAPQEWDVIVVGGGASGLGSAVEAATR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  )<mark>LGFVVPAYDFWAAPFYGIGLKMYD</mark>VLAGKLNLGSSTYLDRDKVLSRVSTYKEKGLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEARAKIVVNATGVWVDDIRRMEDPTVRPMLSPSOGVHVVVEKKFLPGDSAIMIPRTD
                                                                                                                                                                                                                                     ryglnyalwoagelgeravpvoeagralagaegeaaaglktyteearthostlkolaa
hveeleeralkisrvggddislarvrlewroaraariganrleeavqilealvsdsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eaelrhavrhesartvedvlarrtrsillgarasmeaa praaailaeelgkdaawoaq
                                                                                                            MSAPSSPASQDPYRDWLRTRLGREFGVREADQLIQAAVQRRGWQ
                                                                                                                                                                                                             aktahurimijotrspidapapiyuboradopijmididirharysigvpihpnyira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r to PID:1652085 percent identity: 67.48; sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                note="simllar to GB:AE000783 percent identity: 68.44;
dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Product="glycerol-3-phosphate dehydrogenase"
Protein_id="AAF10592.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3228 GAGTACAACGTGGCCCGG . . CCCCAGAGCTGGATGGACCACGTGCAGCC 3182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GlyLeuAspArgGlyGlyGluCysPheProAsnProValPheProSerAs 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
/product="cell division protein FtsH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 4
Percent Identity: 29.661
           10596.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(10120. 12087)
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US-09-151-189-2_COPY_441_676 x AE001953/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to reverse of: AE001953
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ene="DR1019".
                                                                                                                                                                                                                                                                                                                                   'gene="DR1019"
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1.910
51.695
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Percent Simllarity:
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LRGCLLTWIHLMPVAALSLFYGVLLLSTSAAALATLATLSVLRLLVVFPEGLQRVLLT
SYLNLTVTGGSLTQALVLLLIYTLGFSLMAIFAFDRRDL"
complement(2935. 3372)
                                                                                                                                                                                                                                                                                                                                /translation-"wfPigiwieFalricegaricegnLocsdayiaaravachDaFiscw
OGKFEXYNARQS%DDHVDFGRAPSLPPPPFSYPSGRATYSGAAEVLAQFFPLQAR
QLRRDARDAAPSYVVGGTHWGVDGVAGLDVGDRVARALLERRP"
complement (3423 . 4277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           snaaqpsgeglwaplsgqralepgwgrvqpiglapdalpgsrrppagrapsspptas
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hpsilpotograpispavrsciaasplvispaapxirotrsalaaapacbatavo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prryarttldliaarrldpppaaralaltigalhdaaktargsgraydstaaavaa
Rvomalferdgarlaselrsalpplpaevdrasmalggayadavlafaqodgaaqas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar to SP:P25755 PID:45710 percent identity: 11; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="slmilar to PID:1653441 percent identity: 51.76; dentified by sequence similarity; putative"
                                                                                                                                                /product="vanadlum chloroperoxidase-related proteln"
/proteln_id="AAF10589.1"
/db_xref="G1:6458743"
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n_id="AAF10590.1"
f-"GI:6458744"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"ldentifled by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ote="ldentified by Gllmmer2;.putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roduct="hypothetical protein"
rotein_ld="AAF10595.1"
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_ld-"aar10591.1"
                                                                                                      2935. .3372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3423. .4277)
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gene="DR1016"
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NILCIDVRRGIEOTRABETLLARLRDAVSVSDDDDTTRLVSRRIEDLDAAITAKTKLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEGAAWERATRGIDRKALVARLYARRYLADOGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KASWYDRGAGLRQWRSILDMGTVEVFLEAEAPRVNCPTHGPTVVAVPWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ny, e'grigo 157649 in banaceuran degrading confectum (163 aa), FASTA scores: opt. 767 2-scores 296. (): 0, 67.3% identity in 168 aa overlap, or to spision parapertussis insertion sequenc (406 aa), 24.9% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv3798, (MTV026.03), len: 444. Putative
traisposses/Antical to IS1557 MTCV373_32,
sp[010621]103x_MTCTU HYPOTHERICAL 50.2 KD PROTEIN Cv37
(444 aa.,499 8% identity in 444aa overlap and similar
many, e.g.gpl057649]DBU57649_1 bibenznfivrand
                                                                                                                                                                                                                                                                                                        acyl Co. A dehydrogenase similar to E. coll AidB proteingplication of the Assars, scores opt. 455 z-scores 561.5 E(): 9.2e-34. 3 identity in 514 as overlap. Also similar to MTCI356.2 b tuberculosiscosmid (542 as), AidB, 31.9% identity in 514 as overlap. Also similar to MTCI376.2 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAYYLRPDELAFAEPHLIRIGELIGGPVIRWAEETDRNPPRLERYDRWGHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product-"hypothetical protein Rv3798".
protein_ld="CAA1862.1"
db_xref="GI:2950417".
                                                                              possible RBS for Rv3797"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [-"SWISS-PROT:Q10621"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDADCDEALORFDELVAGAFTAEQ1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /proteln_ld="CAA17861.1"
/db_xref="G1:2950416"
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complement(<3382. .4935)
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/note="IS1557-3rd copy"
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/gene="accD4"
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/transl_table=11
physical clone"
60 .64
/note-"possible F
72 .1853
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                                                                                                                                                             "fadE35"
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..(548 aa),
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Submitted (11-70%-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Binxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhillesanger.ac.uk
On Jun 26, 1998 this sequence version replaced g1:2961395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                available on the World Wide Web.

(UKL, http://www.sanger.ac.uk/Projects/A_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of postitional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole, S.T., Brosch, R., Parkhill, J., Garnler, T., Churcher, C., Barris, D., Gordon, S.V., Eiglmeler, R., Gas, S., Barry III, C.E., Tektais, F., Badcock, K., Basham, D., Chillingworth, T., Connor, R., Davies, R., Deviln, K., Feltwell, T., Gentles, S., Bantin, N., Bolroyd, S., Horneby, T., Tagels, K., Krogh, A., McLean, J., Moule, S., Nurphy, L., Oliver, S., Osborne, J., Quall, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23740 bp DNA BCT 24-JUN-1999
In tuberculosis H37Rv complete genome; segment 157/162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adian, with the state of the st
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upstream rlbosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deciphering the biology of Mycobacterlum tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not have predicted the corr
ole we choose an initiation
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                                                                3068 GGCAACTGCGGGGGGGGGGGGGGCCCTTTTCGCGGGTGGCGG 3019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                       3018 GCCATCCACTGGGCCGTGGACGCCGTGGCGGGCCTCGACGTAGGGCAACG 2969
                                                                                                                                                             163 GlylleHisTyrArgPheAspGlylleGlnGlyLeuLeuLeuGlyGluTh 179
146 lyGluIleAsnLysLeuAlaValAsnValAlaPheGlyArgGlnMetLeu 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preceded by an upstream
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If this cannot be identified we choose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplete genome sequence
ture 393 (6685), 537-544 (1998)
(295987
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(1. .>23740
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Mycobacterium tuberculosis
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AL022076 AL123456
AL022076.1 GI:3256026
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ACCESSION
VERSION
KEYWORDS
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AUTHORS
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Percent Identity: 24.432

Thu May 18 22:21:30 2000

gene 8 Ores: Quality: 103.50 Patio: 1.310

alignment\_scores

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... Percent Similarity: 44.886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in 1162 am overlap.
I putative polyketide
                                                                                                                                                                                                                                                                                                                                                                                                  ORF of erya gene
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                                                                                                                                                                                                                                                                                                                                                              len: 1733. Probable
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                                                                                                                                                                                                                                                      DPNAPEAOA IRK SFVENY NLNMA I PWI AAERGF
                                                                                                                                                                                                                                                                                                                                                                                                                  complex polyketide
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milar to m
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Characterization of a Trypanosoma cruzi poly(A)-binding protein and
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rypanosoma cruzi clone 22 poly(A) binding protein mRNA, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
rypanosoma; Schizotrypsnum.
(bases 1 to 2103)
                                                                                                                                              19178 GCTTGTG.......GCGGGGGGGGGGGGCGTTCGTCGCCC 19147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19065 CAAGTCAACTGAGCTTTCCGTCGGCACCACCTCGACCACGGCCGCG 19016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .18958 Arescenterceceaaracrecressescenceacrecceaersarerse 18909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AlaThrValLeuLysAlaLeuIleGlyLeuAspArgGlyGlyGluCysPh 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 eProAsnprovslpheProSerAspAspGlyLeuGluLeuIleAsnPheG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · 138 ludlyAlaCysLeuThrTyrGluGlyGluIleAsnLysLeuAlaVslAsn 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roThrHisProSerTyrProSerGlyHisAlaThrGlnAsnGlyAlaPhe 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 ValalaPheGlyArgGlnMetLeuGlyIleHisTyrArgPheAspGlyIl 171
                                                                                                                                                                                                                21 pGlnValH1sArgPheAlaArgProGluAlaLeuGlyGlyThrLeuH1sA 38
                                                                                                                                                                                                                                                                                                                                                                                                           55 AsnAspGluLeuLeuLysArgValAlaGluIleAsnAlaAlaGlnAsnPr 71
                                                                                                                                                                                                                                                                                                              38 snThrileAlaGlyAspLeuAspAlaAspPheAspIleSerLeuLeuGlu 54
                                                                                                     5 LeulledlyAlaalsGluLeuAlaGlnArgAlaSerCysTyrGloLysTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 oAsnAsnGluValThrTyrLeuLeuProGlnAlaileGlnValGlySerP
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                                                                    to: 23740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19015 GCCTGCTCATGGGCAGAGCCACCGGGCTG......
                                                                 Align seg 1/1 to reverse of: MTV026 'from: 1
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alignment_block:
US-09-151-189-2_COPY_441_676 x hrv026/rev
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Trypanosoms cruzi
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LOCUS TCU11272
DEFINITION Trypanosoma o
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KETWORDS
SOURCE
ORGANISM
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racterization of a Trypanosoma cruzl poly(A)-binding protein and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (02-FEB-1994) John E. Donelson, Blochemistry, University Iowa, 300 Ecksteln Medical Research Bldg., Iowa City, IA 52242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCU06070 2013 bp mRMA INV 16-DEC-1994 Trypanosoma cruzi Tulahuen poly(A) binding protein mRNA, complete
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Bukaryota: Bukaryota: Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum
1 (bases 1 to 2013)
                                                               1085 .....rgrrgrrg... 1077
                                                                                                                                           161 tLeuGlyIleHisTyrArgPheAspGlyIleGlnGlyLeuLeuGlyG 178
                                                                                                                                                                                                                                                                                                                                             193 ... AlaGluGluAlaThrPheGluPheArgLeuPheThrGlyGluValI1 208
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                                                                                                                                                                                                                                            178 luThrileThrValArgThrLeuMisGlnGluLeuMetThrPhe..... 192
                                                                                                                                                                                                                                                                                                                                                                                                         1031 AGAGCGGAAGCGGCAGACACTCAGTTTCATCCTTTCTTTAGCCAATGGAC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 eLysLeuPheGlnAspGlyThrPheSerIleAspGlyAspWetCysSerG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              981 TCTCCTTCTCGTCGAGTTCCTCGACAGCCTTGGCGGCAGCTTCGTGAGTG 932
                                    145 GluGlyGluIleAsnLySLeuAlaValAsnValAlaPheGlyArgGlnMe 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Parasitol. 67 (2):, 301-312 (1994).
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rotein_id="AAC46487.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 931 GCGTACGCGACGTAGGCAAATCCGACTGT 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _xref-"taxon:5693"
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LOCUS TCU06070 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_in2:TCU06070
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AUTHORS
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Lstvlanltpbgoknvlgbrlynhivainpaaa
Direct Submission Submitted (23-JUN-1994) John E. Donelson, Biochemistry, University of Iowa, 300 Eckstein Medical Research Building, Iowa Clty, IA
                                                                                                                                                                                                                                                                                                                                                                                                         77 okslgygynfonpadaekaldoagvklgskhiriakiordpskrrsgythivykf
Lppsvdyyalkemfskygrltaiglatnengesrgyarisyekeesaloayoevngm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1151 ...!.....CITCAGGGGGTGGTGGTGATAGGTCTT 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1288 CCATGAAGCTCCTGGATGGCACGGCTCGCCGCACTCTG......1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1250 .....crccrraaaag 1240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1370 CATGTCTTCCAGTGTCTGGCGACGAGCATCCTTGCGGAG...GGCATATG 1324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :LLDAKVOEALEVLNRHMNV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 gValAlaGluIleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyrL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 SerGlyHisAlaThrGlnAsnGlyAlaPheAlaThrValLeuLysAlaLe 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ulleGlyLeuAspArgGlyGlyGluCysPheProAsnProValPheProS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 AspalaAspPheAspIleSerLeuLeuGluAsnAspGluLeuLeuLysAr 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HisTyrPheArgLeulleGlyAlaAlaGluLeuAlaGlnArgAlaSerCy 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 euleuProGlnAlaileGlnValGlySerProThrHisProSerTyrPro 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 ......LeuGlyGlyThrLeuHisAsnThrIleAlaGlyAspLeu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: ICU11272 from: 1 to: 2103
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0.933 Gaps: 11
43.210 Percent Identity: 22.634
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rotein_id="AAC46489.1"
                                                                                                                                        ...2103
'organlsm="Trypanosoma cruzi"
'db_xref="taxon:5593"
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US-09-151-189-2_COPY_441_676 x TCU11272/rev
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Ratio:
Percent Similarity:
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                                                                                                                                        Source
   TITLE
JOURNAL
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                                                                                                          FEATURES
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.......CITCAGGGGTCGCTGGTGACAGTACGTCAAAGTTCTT 1025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 erAspAspGlyLeuGluLeulleAsnPheGluGlyAlaCysLeuThrTyr 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 tLeuGlyIleHisTyrArgPheAspGlyIleGlnGlyLeuLeuGlyG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 ... AlaGluGluAlaThrPheGluPheArgLeuPheThrGlyGluValil 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        988 .. ACGTCGCGGCGCAGACGTTCGCGCTCGCGTG... ACGTTCATCTCG 944
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                                                                                                                                                                                                                                                                                                                                                                                             1235 TCACAAAAAGTGG......acGCGGCCCAAGGCCCGTGCTT
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                                                   Gaps: 11
Percent Identity: 22.22
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                         Length:
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US-09-151-189-2_COPY_441_676 x TCU06070/rev
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                                                   Ratio: Percent Similarity:
alignment_scores
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seq\_name: gb\_inl:AF044733

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(26-7AN-1998) Biologia Celular, Universidade de Brasilia, Iversitario - Asa Norte, Brasilia, DF 70910-900, Brazil Location/Qualifiers
   AF044733 4292 bp DNA INV 11-FEB-1998
BIYPANOSOMA CTUZ1 Glone BIX POLY(A)-binding protein (PABP) gene,
                                                                                                                                          Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secondary spliced leader acceptor site"
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Gaps: 11
Percent Identity: 22.222
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1-"AAC02538.1"
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strain-"Dm 28c"
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Satista, J.A.N. and Martins de Sa, C.
pirect Submission
                                                                                                                                                                                                                                                                                                                                            complement(781. 1102)
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                                                                             AF044733.1 GI:2854067
                                                                                                             Trypanosoma cruzi.
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seg_documentation_block:
LOCUS AF044733
DEFINITION Trypanosoma o
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AUTHORS
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                                                             ACCESSION
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KEYWORDS
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Submitted (26-JAN-1998) Biologia Celular, Universidade de Campus Universitario - Asa Norte, Brasilia, DF 70910-900, Location/Qualifiers
       Euglenozoa; Kinetoplastida: Trypanosomatidae
                                                                                                                                                                                                                                                                                                                                                                                                                           secondary spliced leader acceptor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1776 CARGIGITECAGIGITEGGGGACGAGCAICCTIGGGGAG...GGCAIAIG.1730
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Gaps: 11
Percent Identity: 22 222
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strain-"Dm 28c"
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                                                                     and Martins de Sa, C.
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US-09-151-189-2_COPY_441_676 x AF044732/rev
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                            Schizotrypanum.
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/gene-"PABP"
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5238. .5270
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/gene="PABP
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Source
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AUTHORS
TITLE
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                                                                               3494 CATGITCCAGIGICIGGGGAGGACCAICCIIGGGGAG...GGCATAIG 3448
                                                                                                                                                                 3447 TCACAAAAAGTGG.....ACGCGGCCCAACGGCCGTGCTT 3413
                                                                                                                                                                                                                                                                                                                                      .....CICITIAAAAG 3364
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    to: 4292
Align seg 1/1 to reverse of: AF044733 from: 1
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LOCUS AF044732
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KEYWORDS
SOURCE
ORGANISM
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TITLE The sequence of IAC TUPBH12 from Arabidopsis thaliana chromosome I JODERNAL. Uppublished (1997) REMARK. We have determined that YAC yUPBH12 is chimaeric, and is comprised of two distinct genomic EcoRI fragments from chromosome I This submission contains the sequence from the EcoRI site at position 181919 to position 285516 (left end) of our previous phase II submission. This fragment contains the AXRI locus and the marker YUPBH12L.  YUPBH12L. (YUPBH12L.) AUTHORS Theologis, A.		Street, Albany, CA 94710, USA 5 bases 1 to 103576) Theologis. Direct Submission 3 bant Gene Expression Center, Submitted (10-SEP-1997) Plant Gene Expression Center, CA pany, CA 94710, USA 6 (bases 1 to 103576) Theologis. Direct Submission Submitted (12-SEP-1997) Plant Gene Expression Center, Submitted (12-SEP-1997) Plant Gene Expression Center, St. Albany, CA 94710, USA 7 bases 1 to 103576)		/clone="supering page   1	//Trablation-WakeRegNorthstyVesDookrafth.KhebyLikuchartovaku. VGFELAIKADDAYKAAKQLRSCLSKTASCISTERLAKHSPYLIKUCHARTOVAKU. VGFELAIKADYYKAAKQLRSCLSKTASCISTERLAKHSPYLIKUERETUAYDLILCKSTAHLPFFF PFITTATRALLALISTSHEHTOTTONSRGARTFYORDESTAMINSMODFQDSTOVE DFSSSYPSRVSSIRFDESSLRSTRFATVSRCGLATMINSMODFQDSTOVE DFSSSYPSRVSSIRFDESSLRSTRFATVSRCGLATTTDRISIGTIR DPRIPRSFSTGPALFFRESTSSLRSTVSKSERFRFYORDENTYRSKMRPPLC GLOWFLWSTOTATRRINSLSCGN*  GOMPLEMENT (8774. 8453,8547. 8726,8824. 8940, complement (8774. 8453,8547. 8726,8824. 8940, 10691. 10736) /gene="TUP8H12." /gene="TUP8H12." /gene="TUP8H12." /gene="TUP8H12." /note="Similar to Arabidopsis hypothetical protein  PID:e325639 (gb 297337)."
17 styrclnLystrpGlnValHisArgPheAlaArgProGluAla	gvalAlaGluIleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyrL	111   ulleciyLeuAspArgciyciycyPheProAsnProValPheProS   128	theudivileRisTyrArgPheAspdivileSe	1437 AGAGGGAAGGGCAGCACTCCATTTCCTTTT	seq_documentation_block: LOCUS VUPSHI2 103576 bp DNA. PLN 29-SEP-1997 VUPSHI2 103576 bp DNA. PLN 29-SEP-1997 Arabidopsis thaliana chromosome 1 YAC YUPSHI2 complete sequence. ACCESSION AC000098.1 GI:2358139 VERSION AC000098.1 GI:2358139 RTG. Arabidopsis thaliana ORGANISM Arabidopsis thaliana ORGANISM Arabidopsis thaliana Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; eudicots, Rosidae, eurosids II; Hrassicales, Brassicaceae; Arabidopsis. Arabidopsis. Arabidopsis. Arabidopsis. Theologis, Arabidopsis. Toriumi,M Yu,G.; Oji,O., Araujo,R., Chung,E., Dewar,K.,

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jóin(23118. 23497,23582. 23753,24134. 24340,24432. 24691,
24781. 24937)
/gene="YUPBH12.7"
BELDOSSAENELLADTNNOLK IKIOELEGYLOSEKETA I EKLNOKDTEAKOLITKLKS
HENVIEEHKROVLEASGVADTRKVEVEEALLKINTLEST I EELEKENGOLAEVNIKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVOSAVDAVGESORRNVIMINSGIEKVVIPKTKPNITLOGGGFDITAIÄMNDTAYSA
NGTFYCATVOYFGSOFYAKNISFWÄNYAPIPKRGDVGAQARAIKIAODESAFYGGFFG
AGDTLADDRGRHYFTDCTIGGSIDFIFGNAKSLYODCRIISMANOLSPGSKAVNGAVT
ANGRSSKDENGEPEVRGTIGGTGHWALGRAWFYSKYVEYSTTWTDVIAPEGNNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /teanslation-"mrttonktllefffftsesleffthydgeskoecsheddeankad
akktytalesuladolughgffeslepestfffytherakaladebhu
leboteklispelladebfffthavaalillendebhus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEBODAGGGGGGGDELGLHVHAHGHTHGIVGYESGESOVOLHRTRVVAQVLEVGIIVH
SVVIGISLGASOSPDTAKALFAALMFHQCFEGLGLGGCIAQGNFNCMSITIMSIFFSV
                                                                                                                  IHLKEEVEKVAELTSKLQEHKHRASDRDVLEEKAIQLHKELQASHTAISEQKEALSHK
                                                                                                                                             hselratlkksqeeldakksvivbileskingleokvkladakskvshikhnifkpni
Oetestgreeevevksrdsdlsfsnprotrikknidaasssghvmiokaetwhlatlk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="mkiislsisigialiavlasktlekthpeafgikaisysfkksl
                                                         OKLANOGSETDDFQAKLSVLEAEKYQQAKELQITIEDLIKQLISERERLRSQISSLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDRHHHHHHHHHHHHHPBKPSDIKRKVSICDDFPKNIPPLDTDTISYLCVDKNGCCNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPSRDATIFYGEYNCSGPGADMSKRAPYVQKLNETOVALLINTSFIDGDQWLQFSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Similar to Arabidopsis Fe(II) transport protein
                                                                                                                                                                                                                                                                                                                                                                           /note-"Similar to Prunus pectinesterase (gb|X95991)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4/045. .30294

/gene-*TUPBHIL2.8

1041(27848. .28469,29215. .29364,29989. .30294)

/gene-*TUPBHIL2.8*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92333 CTAACGITATCIICGCIIACGCIATAAICIITACICAAGIGGIAICIGII 92284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92283 GGATTACCAGTTCAAGAATCTTTTCCT.....GG 92255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92383 GARICGACGAITITGGAIAGAGIGAITGITITCAGCIGGAAITGICG 92334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92254 AGIICITGITCCTGAIGITAAGICITICICIGCTGCTICICGIGAIGGA. 92206
                                                                                                                                                                                                      IALGVALVSVILGI: IICLFDCFVVLRIFASTILLFLIDQARPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 yAlaPheAlaThrValLeuLysAlaLeuIleGlyLeuAspArgGlyGlyG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 luCysPheProAsnProValPheProSerAspAspGlyLeuGluLeuile 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 uAsnaspGluLeuLeuLeuLysArgValAlaGluIleAsnAlaAlaGlnAsnP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 AspleadspaladspPheAsplle....SerLeuleuGl 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 roAsnAsnGluValThrTyr....LeuLeuProGlnAlaIleGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: YUP8H12 from: 1 to: 103576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 219
Gaps: 9
Percent Identity: 21.461
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_id="AAB71447.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                    //dence-not_experimental
cotein_id="AAB71446.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-151-189-2_COPY_441_676 x YUP8H12/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAB71447
/db_xref="G1:2388566"
                                                                                                                                                                                                                          23118. . 24937
/gene-"YOP8H12.7"
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0.979
42.922
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                       gene
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12540,12819 12954,13147 13183,13265 13347,
13472,13525 13559,13734 128068,13929 14015,
44239,14357 14409,14513 14661)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   v.coms.lation="MSOYDHYOSAGANPPPPMSTCTSPPPPIGFFNOPSHGSVAGGK
VETKSGDGFFKGCLAAMCCCCALDICF"
Complement(16969, 17382)
                                                                                                                                                                                                                             SRABALSGGRAKELEFCSGDDAGFIAKRYROIKSFFLEBSOYLAFFTILILASYPPP
FDLAGIMGGOPERPFWEFFLATLIGKAIIKTHIOPYFILCOKNOLLOPVENELIYI
SFVBRASHLELIAKLKHARRITIASPPSSDINVTKRIDLSERASYNGYYHLMLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ttanslation-"MadhnaTPPFDLTRLDHIIKYOPRERAEDFVHVEVKVLGKGSS
PLEISFSTSYTEFVWEDEDCYELVELYEFFTEDAGIDAFEAGFLVNDLILKYNKTTRP
LDEDFFYFVFKLAMEYTIKFVQLNHAGSGKTESGQP"
COmplement (17782. 20696)
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EALOVRINSILENILE VAMEREPOLESKIAN YMERIKASSEERLEKOOREIDEATTRISIE
LEALHKHSELKYOKTWEDPSSROFEARSLIFRSKOLEER KRYTEGKLAEACGOSISKLO
                                                                                                           MGYGNRASSKIPAISGLREKHOODLEKLILISOPPKILRLFVVA
                                                                                                                                      felyvrrnssyllannghlilecsifvaraallytlophykyrktykfsnfllyohy
belseytreglwuiflgvassiglgsglhyfylylgphialftikvwqcgrvdlksai
                                                                                                                                                                                                      IEAILWGLGTALGELPPYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaslpttmgvvagllvonslkellinfgevsptilgtnslköppptmkmrpnpocsnva
.erokeymlakperdaaakarmeadasttidegplhddnewnisvvddenekdttka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iote="ESTS gb|AA042402.gb|ATTS1380 come from this gene."
codon_Start=1
voidence=not_experimental
protein_id="AAB71445.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKSLEELSEKVSELK$ALIVAEEEGKKSSIQMQEYQEKVSKLESSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .on="mevgfkallddldvlekslsdpalinklrshvenlatlskcnph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOGFETFTSSLTNKSFCPSKEGGSGVDLVLSCVDNTEARMAVNOACNELROTWMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tt(join(17782. 17868,17912. 18142,18194. 18376,
8607,18685. 18894,18966. 20600,20652. 20696))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .on="meertkvssdvpgakflekikycddlloevtkedtvmekeedt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEEKLKISDERYSKIDALLSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Similar to Caenorhabditis unknown protein T03F1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assotlpeglirelpvadetekaiaiasgsgeteeeddlkkolealnaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oin(15906. 15936,16035. 16176,16428. 16473)
gene-"YUP8H12.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ote-"EST gb|ATTS0295 comes from this gene." odon_start-1
                                                                                                                                                                                                                                                                                                                 FGOIVTSTAORYLKKOOEEELDALTNKSSLISKKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /idence-not_experimental
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rotein_id="AAB71443.1"
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                                                                                                                                                                                                                                                                                                                                                      547. .14561
ene="YUP8H12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5906. .16473
gene-"YOP8H12.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAVSCHIO
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us-09-151-189-2\_copy\_441\_676.441-676.rge

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/translation-"MSMFSAKELINIAVRYEKEGEEFYRXIAERFTQPDIKEFFSYMS
ROEAEHARFEEKGEEVGAKEETYLDHEDFERLKSFVEGKEFPSPEVMRYIKEKSV
BEAIDFSISVEKETIIFYYEILELKKNEKARSLVKGIIEDEKOHVYKLLRIKGMIT"
COMPLEMENT(1.129...3049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPOPHERNYAVOT FGSEPNELSEATILSEKTRNIDLNAGCPVRKVVKKGAG
LEMERYTVRELEKSYGGEFSVYKTRLGFRENEVELT RILVEGEVDEV HYR
TGRBETALSVLEKTPTPVSODITTPEPDAKRALEESGCOGILVARGAIGR
KDFIRSGRYSEPSREDILRTFERHLELLIKTKGERKAVVERRKILAGYTKOL
                                                                                                                                                                                                                                                                                                    /translation-"mniibyliviaiskmimgffiptimfkegkdhqavafkvwfirm
IERTSRNGLLIIEDNGKIVTYDDHKNEKKIYEFPFIFLSKVAVDGEDITFKNGFVSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation-"MPTXTVAVEGSGKKITGVIEAENKLKAISILSERGLMVVRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKSAMAYPLFVLFFAVVIVLVISFYILPNLVRAFGTSIPLSPTIRSLLKANEFLSENW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGYRITDAIKWAAQASSPSIIRKTEEMYRKISEGKTLRDTFAESGYFPQLIYENIGT
GEETGKYDEVÆRRYADFYEDIVKNSYRQLVSLVEPLLIAGVGGFVAFLAYSIYTYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *MEVKVGLAPMAGYTDSAFRTLAFEWGADFAFSEMVSAKGFLMNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKKAQRSSTRFOISISEIATFCRQLSIMISAGIRIKEALNILARQTVFSRRFRKVILE
                     /note-"similar to percent identity: 0.00; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="general secretion pathway protein F, putative" (protein_id="AAD35188.1" (db_xref="GI:4980584")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:AE000557 percent identity: 58.04; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"similar to GB:AE000657 percent identity: 58.28; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.12;
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GB:AL009126 percent identity: 55.41; identified laguence similarity, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /hote-'similar to GB:Pyro_h percent identity:
identified by sequence similarity; putative"
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/protein_id="AAD35189.1"
/db_rref="GI:4990585"
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/protein_id="AAD35190.1"
/db_xref="G1:40a^r.??"
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/protein_id="AAD35191.1"
//db_xref="GI:4980587"
                                                                                                                                                                           /product-"hypothetical protein"
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/db_xref-"G1:4980583"
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/gene="TM0095"
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Center Dr., Rockville, MD 20850, USA
Location/Qualifiers
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K.D., Garrett, M.
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                                                                                                                                                                                                                                                                                                        92107 TCCGGAGCACAATGTCTTGCTCAGGATCGAAAGAGGGAAGGAGTTTCG 92058
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    ..TIGCTICCGGGAGATGTTATCTTAGCCGTTGATGGTACTGAGCTATCT 92158
                                                                                                                                                  32157 AATTCCGGTTCTGATTCGGTTTCTAAAGTTGTTGATGTTGTGAAGAAGAA 92108
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                                                                                                                                                                                                                                                                                                                                                                                 ......PheGluGlyAlaCysLeuThrTyr 144
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enome sequence of Thermotoga maritima
399 (6734), 323-329 (1999)
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Locus AEO01696 15113 bp DNA
DEFINITION Thermotoga maritima section
ACCESSION AEO01696 AEO00512
VERSION AEO01696.1 GI:4980582
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/translation-"mkkhiflelifilvupvisyaidienvtaofokluedyesgepod
Ppvsyvkentpolokyrifrrplagsvektepaktpgdylevlyonwketnwerkisn
Yleissylogskigspesesvikneparnsperatranvershilmilatyfget
Tpppvedhildipptgsprnundvihofilkuptoen.
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PID:516592 PID:1753225 percent identity: 56.65, identified
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                                                                                                                         GPSFNVNHDVHPDILKVLPEDLEAKLKEAIEEIASSKNQAEYTF
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KIEGDLSDYLSQEKSRYRKRREINSLDQLIKKITSYTSEKFSQDFERELTNTIERYF
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                                                                                                                                                                                                                                                                                                                <u>LSMIKWKNIEVFVESGIFPLIIETSSTHTFHIEVFLIFVSLFLLYKNFMKRRVKA</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10226 CGGATCTTCGAAATCCTGTGTGTAGCCTCTCAAGATTTTCACGTTCTTTT
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Gaps: 11
Percent Identity: 21.849
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US-09-151-189-2_COPY_441_676 x AE001696/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10053 ACCCACCAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reverse of: AE001696
                                                                                                                                                                                                                                                                                                                                                /gene="TM0102"
9654. 1077
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/translation="MLSGSETSSLATGNRIGIFGGSFDPVHTGHVLVSVYTLEILDLD
FLIVVPPYRRPHRATVAPPERRENEMKKYPEGGHRKAEVSPETERGGVSYSIFTIEVP
SELIVILDMPTVOISSTEIRERARIGKTILGFYPEEIRKEVEVFYGG
EIVPLDMPIVOISSTEIRERARIGKTILGFYPEEIRKEVEVFYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        radslation-"megmelifbgrplkspcpsnypnighrheppelrgsllrtfddl
ilkreldbyyddrhidaefsklkvwgtsdeaeslleavhkvlalppqifleiggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGILKKELPEYEDVSKHIDAESKLKVWGSSDEABSLLEXVHKVLALPPOIFLEIGG
LIFSVAGARKSEVLKELEKNKFPRSKAPVRITRPRIFFKTPLISKETIFLSFLK
SPAGEVFLELSAGDRIHGKNFLSPFHEISKKDDRFKASLAKDLEITESTVOLLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLERPEIVVANKIDLIGKEELEKILKRIRDATNREVIPVSAVTGEGIDLLVSKLASIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ranslation-"mserkipkevieeverlreeieyhnyryyvundpvitdeeydrl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="similar to percent identity: 0.00; identified by equence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"similar to GB:AE000657 percent identity: 69.80; dentified by sequence similarity; putative"
                                                                                                                                                                                                                      /note="similar to GB:AE000657 percent identity: 73.19;
doubtilled by sequence similarity; putative"
/codon_atart=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORDARLMILOVLERNGLNNKLREAGVKEGDVVRIGDFEFETRE
                                                                                                                                                                                                                                                                                                                    product="conserved hypothetical protein"
/protein_id="AAD35192.1"
/db_xref="C1:4980588"
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rotein_id="AAD35193.1"
b_xref="GI:4980S89"
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protein_id="AAD35195.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="DNA ligase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4917. .5690)
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                                                                                                                complement(3613. .4920)
                                                                                                                                                                      complement(3613. .4920)
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trans1_table=11
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7780
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                                                                                                                                                                                             'gene-"TM0098"
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/gene="TM0101"
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70D_XTEE=TRUSS-FRANCHINGSPAINS
/translation="Mintiligalateslyydkrensiflyllilelvfiivspains
kntestvedipshkarnvykkrleleotlosilnkntssid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MXLDVPYYRLGNHEKVEYIPLKLALNDDTASEPQOFSEPVHKMP
INDMGGYDNTTSMVSAGIIILISVVAFIALFLLLYVIYYFVILREQQQYSDSIDTDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xiee--spiss-prot.co6692"
/translation-imalitytrykvyilrodngkytkirlikarpellinkfilan
Kclrnathirlingsatokytamakytiikkoskytkirlikarpellinkfilan
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Vddinvlikrgklesdtinjkrkksrnntlikmirlelareiysrnptiloisknt
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YLNKYNIGLDETSSEEENNNDDDDAQHNRNSSGSSGESLLYYRNE"
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HVSTGYSFEFHPGSQPRTEQTIHTDGLIIKVLILCDECCKKELRDYIKGENSFNVAFR
NCESILCRRVSFQTVLLTCAILLLENVEKFSMINLLIILLILSLFCHNNYIISNPY
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                                                                                                                                                                                                                                                                                                 nnslwskymppkpfapttlksyksrfikivycsvddvhled
                                                  ISS-PROT: 006690"
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                                                                                                                                                                                                                                               'db_xref="SWISS-PROT:Q06687"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2419. 3648)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'protein_id="Caa50541.1"
'db_xref="G1:296324"
  /protein_id="CAA50539.1"
/db_xref="GI:296322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               b_xref="G1:296326"
                                                                                                                                                                                               protein_id="CAA50540.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="CAAS0544.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1770 .. 2099)
/note="ORF 327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2102. .2416)
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/citation=[3]
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/citation=[3]
/replace="at"
3949
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Whitford,M. and Faulkner,P.
Whitford,M. and Faulkner,P.
Whitford,M. and Faulkner,P.
Wholeoritde sequence and transcriptional analysis of a gene encoding gp41, a structural glycoprotein of the baculovirus Autographa californica nuclear polyhedrosis virus
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ikikrvvnmfinnelennkiyklvetvdssnkisrrqvdfihallnnvsvtftlhrf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORF 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ubmitted (14-APR-1993) D. Zuidema, Agricultural University ageningen, Dept of Virology, Hinnenhaven 11, 6709 PD Wageningen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Autographa californica nucleopolyhedrovirus" /strain="Achinpv-E2"
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Rool, M., Broer, R., Zuldema, D., Goldbach, R.W. and Vlak, J.M.

Rool, M., Broer, R., Zuldema, D., Goldbach, R.W. and Vlak, J.M.

Nuclectide sequence and genetic organization of a 7.3 Kb region

[map unit 47 to 5.5.5 of Autographa californica nuclear

polyhedrosis virus fragment EcoRi-c

J. Gen. Virol. 75 (Pt 3), 487-494 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein gp41; ORF 1137; ORF 141; ORF 1728; ORF 201; ORF 208 785 235; ORF 235; ORF 282; ORF 312; ORF 312; ORF 339; ORF 312; ORF 339; ORF 913; ORF 339; ORF 201; ORF 339; Autographa californica nucleopolyhedrovirus
Autographa californica nucleopolyhedrovirus
Yuruses; GabNa viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ACMPVDNA 7297 bp DNA VRL 17-FEB-1997
Autographa californica nuclear polyhedrosis virus DNA.
X71415
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On Aug 6, 1994 this sequence version replaced g1:296320.
Location/Qualifiers
                            9931 ACTITAAAGAGATCATTCGTCATGAAACCAACAACGGAACACGGGATC 9882
                                                                                                                                         9881 AGCTTCTTCCGCTGCTTTGCTGAGGTTCGGTATGTAGTCGGACTGCTCGT 9832
                                                                                                                                                                                                                                         9831 AAGATIGTATCAC.....TITCGCTTCTATTCCGAGTTCTTCTGCG 9791
.....HisGlnGluLeuMetThrPheAlaGluGlu 195
                                                                                                  .GluPheArgLeuPheThrGlyGluValII 208
                                                                                                                                                                                            208 eLysLeuPheGlnAspGlyThrPheSerIleAspGlyAspMetCysSerG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erratum:[[published erratum appears in J Virol 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of ACMNPV DNA
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ap="47 to 52.5 map units
mplement(1. .339)
ene="ORF 339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "CAA50538.1"
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/gene="ORF 339"
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                                                                                                                                                                                                                                                                                                                        9790 GCCTGCTTTATTCC 9777
                                                                                                                                                                                                                                                                                         225 lyLeuvalTyrThr 229
                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_v1:ACNPVDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
S ACNPVDNA
                                                                                            196 AlaThrPhe....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
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MEDLINE
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AUTHORS
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REMARK
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AUTHORS
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sytochrome oxidase subunit I.
Yrorocentrum micans (strain:NIES12) mitochondrion DNA.
Altochondrion Prorocentrum micans
Sukaryota: Alveolata; Dinophyceae; Prorocentrales; Prorocentraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases. Yuji Inagaki, Biohistry Research Hall, Molecular Evolution Laboratry; Murasaki-cho 1-1, Takatsuki, Osaka 569, Japan (E-mail:Yuji.Inagakielms.brh.co.jp, Tel:0726-81-9761,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLN 05-FEB-1999 Prorocentrum micans mitochondrial DNA for cytochrome oxidase amonna, I, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5896 ......Greccac 5912
                                                                                                                                                           5688 ATGCATAGATTTACCCAAC......GGTACGGCCAACATGTAT 5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5869 ......TTCCCAACTGAGGTGTTT.......GACGGCACC..... 5895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5913 CGCGGACAATGTCAACTTTTTACGTTCCACGTTTGCCATTGAAAATATTC 5962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6060 CATCTTTGCTCAATGGCTTTTGTATGCGAGAGACAAAAACACCCATCGGGC 6109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5726 TCAAACACGTTGACGACGATATTTCGTACAACAGTGGCCAATTGGTGTGC 5775
                                                                                                                                                                                                                                                                                                                                                5963 CARACCATTATGGCATCGAC. .ATGCAAACCACCATGTTGGGCACGACC 6009
                                                                      5638 AACCGGATCAGAAACTCTGACAACCAGTACGAGTGTTCCGACGACTCCAG 5687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 uAlaValAsaValAlaPheGlyArgGlaMctLeuGlyIle.....164
                                                                                                                                                                                                                                                                                                                                                                                             104 eAlaThrValLeu......LysAlaLeulleGlyLeuAspArgGlyG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 lyGlucysPheProAsnProValPheProSerAspAspGlyLeuGluLeu 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 .... HisTyrArgPheAspGlylleGlnGlyLeuLeuLeuGlyGluThr 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 IleThrvalArgThrLeuHlsGlnGluLeuMetThrPheAlaGluGluAl 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 .......PheThrGlyGluVallleLysLeuPheGlnAspGlyThrPhe 216
                                                                                                                                                                                                                                                                                                      79 .....LeuproGlnAlalleGlnValGlySerProThrHisPro.
                                                                                                                                                                                                                                                                                                                                                                                                                                       5826 TGAAAACGCGTTGTTATGGACAAATTTAGATTAAACATGCAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6010 GAAATGGTTAAACAGTTGGTTTCCAAAGATTTGTCGTTAAACAACGACGC
                          66 AsnAlaAlaCinAsnProAsnAsnGluValThrTyrLeu......
                                                                                                                                                                                                       92 .....SerTyrProSerGly....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 aThrPheGluPheArgLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B000134.1 GI:2897831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pll:AB000134
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Locus AB000134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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AUTNORS
TITLE
JOURNAL
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KEYWORDS
                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="SptremBL:064811"
'translation="MHAFVIGGRVDGIEPRYNISVLHNIRHVAYYVGCGFVCYGALHI
                                                                                                                                                                                                                                                                            /aspolrllyknaystvscgnygvicnlvongerdlnaimfncaetrlnkgomlf
Kinrednsktdaavhtsepkrtvetendddgraasaaaideoegnadvygldpeen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5591 ATTCAAATGTTTGAATAATAACCAG...TCACAACTGATAACGTGCATC 5637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5512 TCGTGCGTGCAA......GCGCATCCGTGCGCGTT 5540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5541 TAACGCGCCGGACACACGTACATAACGCCCGATATCGGCGACACGCAAT 5590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 uGlyGlyThrLeuHisAsnThrlleAlaGlyAspLeuAspAlaAspPheA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 spileSerLeuLeuGluAsnAspGluLeuLysArgValAlaGluile 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 SerCysTyrGlnLysTrpGlnValHisArgPheAlaArgProGluAlaLe 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 14.206
                                                                                                                                                                                                                               xref="SWISS-PROT:006691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 7297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       odon_start=1
rote1n_id="CAA50546.1"
                                                                                                                                                                                  "CAA50545.1"
                                                                                                                                                                                                                                                                                                                                             mplement(4586 . 4729)
ote="ORF 141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSHHLEPLGESRFVKFKINCOIN
1607 c 1599 g 21
                                                                                                              4730)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4753. .4956)
/note="ORF 201"
                                                                                                                                                                                                                                                                                                                           GDAPTPKKOKLDNAKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allgnment_block:
US-09-151-189-2_COPY_441_676 x ACNPVDNA
                                                                                                              mplement(4188.
                                                                                                                                                                                                                                                                                                                                                                                             5. .5507
te-"ORF 810"
/citation=[3]
                                                                    citation=[3]
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0.774
44.841
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 1943
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                                            conflict
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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221 spMetCysSerGlyLeuValTyrThrGly 230

787

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ellates as inferred from mitochondrial sequences
Evol. 45 (3), 295-300 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 CAACAGGAATAATTCTTGGAAATGCAGCAGTGGATCTAGGATTACATGAT 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 HisProSerTyrProSerGlyHisAlaThrGlnAsnGlyAlaPheAlaTh 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 CATCATATGTATACTGTAGGTTTAGAAACTGATACAAGACCTTATTTTAC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 rvalLeuLysAlaLeuIleGlyLeuAspArgGlyGlyGluCysPheProA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 snProvalPheProSerAspAspGlyLeuGluLeuIleAsnPheGluGly 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574 TGGTTAAGTACATATCTTGGGAATCTGCCATTCTTACAGCTCAAAACTAA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 nvalalapheGlyArgGlnMetLeuGlyIleRisTyrArgPheAspGlyI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       624 ITCAGCATICITIGGACTICITITIATIAATGITTACTATAGGIGGCT 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 leGlnGlyLeuLeuLeuGlyGluThrIleThrValArgThrLeuHisGln 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 GluLeuMetThrPheAlaGluGluAlaThrPheGluPheArgLeuPheTh 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          724 ..... ACATATTATGTTGTAGCTCATTTTCATTTTGTTCTTTT 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 rGlyGluValIleLysLeuPheGlnAspGlyThrPheSerIleAspGlyA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AlaCysLeuThrTyrGluGlyGluIleAsn.....LysLeuAlaValAs 154
                                                                                                                                                                                                                                                                                                                                                                                                                                  oxidase subunit I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 143
Gaps: 4
Percent Identity: 25.175
                                                                                                                                                                                                   /organism="Prorocentrum micans"
/organelle="mitochondrion"
strain="NIES12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AB000134 from: 1 to: 909
                                                                                                                                                                                                                                                                         lb_xref-"taxon:2945"
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US-09-151-189-2_COPY_441_676 x AB000134
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality: 87.00
Ratio: 1.338
Percent Similarity: 45.455
Fax:0726-81-9757)
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                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                        JOURNAL
MEDLINE
FEATURES
               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                gene
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126.61
126.61
123.47
117.63
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US-09-151-189-2_COPX_441_676 x V56020
                                                                                                                                                                            seq_documentation_block:
ID v56020 standard; cDNA; 1794 BP.
73.00
73.00
73.00
73.00
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2.276
63.839
                                                                                                                             seq_name: N_Geneseq_36:V56020
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Quality:
Ratio:
Percent Similarity:
N_Geneseq_36:N40180
N_Geneseq_36:N20043
N_Geneseq_36:V00292
N_Geneseq_36:V69792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                       re Len | Documentation | 1948 | Haloperoxidase, CP.BP01 encodi | 1994 | Haloperoxidase, CP.BP02 encodi | 1994 | Haloperoxidase, CP.BP02 encodi | 2088 | Chloroperoxidase CDNA Use of | 2088 | Chloroperoxidase CDNA Clone 6. P | 138894 | Achary genomic DNA clone 6. P | 13894 | Chloroperoxidase gene. Enzymat | 2822 | Curvularia werruculosa halopex | 1830 | Continuation (12 of 17) of | 375 | Servatia marcescens IAM 1346 a | 375 | Servatia marcescens IAM 1346 a | 375 | Servatia marcescens IAM 1346 a | 4592 | Servatia marcescens IAM 1346 a | 4592 | Servatia marcescens IAM 1346 a | 4592 | Helicobaccus pneumoniae genom | 7577 | Streptococcus preumoniae genom | 7577 | Streptococcus pneumoniae genome | 7577 | Streptococcus pneumoniae | 7577 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 | 757 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fabroblast growth factor receiverations of the factor receiped bus sequence of particle bus encoding sarcesine oxidase
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Drosophila Timeless gene prote
TIM splice variant coding seque
Drosophila Timeless gene prote
Lycopene cyclase gene. Novel I
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! Continuation (17 of 17) of
DNA seqeunce of pKKtdC238Mtb.
! Sequence encoding mannuronan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus sarcosine oxidase gen
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                                                                                                                                                                      Command line parameters:
-MODEL-frame+LpI, model. -DEV-Xlp mod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cterial
     out_format
                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64976
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OM of: US-09-151-189-2_COPY_441_676 to: N_Geneseq_36:*
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143.24
365.49
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0.6653
0.6653
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1.1e-29
8.6e-29
0.9831
301.07
0.8179
2.66
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25.31
49.20
0.7603
1.39
1.39
1.39
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1.0.10
1.70.93
47.93
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25.48
19.07
25.90
25.98
108.59
10.38
10.38
47.63
64.77
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325.50 669.57
328.00 653.40
87.00 152.82
86.50 149.63
86.50 155.00
85.50 151.07
83.50 141.88
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Oucary: US-09-151-189-2_COPY_441_676
Oucary length: 236
Database: N_Geneseq_36:*
Database sequences: 311585
Database sequences: 31585
Database length: 125096042
Search time (sec): 59.880000
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N_Geneseq_36:Y21209_
N_Geneseq_36:V54702
N_Geneseq_36:Q63293
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Sequence
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| Sequence of recombinant CGF | Pre-prorentin-A gene DNA se | Insecticidal protein encodi Candida albicans canity 9en
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VSS020:
09-DEC-1998 (first entry)
Haloperoxidase, CP.BP01 encoding cDNA.
Haloperoxidase, CP.BP01 encoding cDNA.
Haloperoxidase, enzyme; CP.BP01; CP.BP02; vanadium; halide specificity;
Haloperoxidase; enzyme; CP.BP01; CP.BP02; vanadium; halide specificity;
Haloperoxidase; enzyme; CP.BP01; CP.BP02; vanadium; halide specificity;
Horonine; iodine; ds.

Corallina pilulifers

1. 1794.

1. 1794.

Aproduct- "Haloperoxidase, CP.BP01"

/note- "the stop codon is not indicated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1188 ACGGTACCAGAAGTTTAACATTCATCGTCGCCTGCGCCCTGAGGCTACCG 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCTGAGGTTGATCTTGCTGTTGAAGACTTGGAGATATCTTGGAGAA 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGATCCTTCATTCCTGTTGCCGATGCCATTCCCCGAGGCAGCCCATTC 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HisTyrPheargLeuile. .. GlyalaalaGluLeualaGluArgAlaSe 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 rCysTyrGlnLysTrpGlnValHisArgPheAlaArgProGiuAlaLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 lyGly...ThrLeuHisAsnThrIleAla.....GlyAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 AspalaAspPheAspIleSerLeuLeuGluAsnAspGluLeuLeuLysAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9ValAlaGluIleAsnAlaAlaGlnAsn.....ProAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1338 AGCTGAATTAGCAATAGGAAGCAGAACATAGCTGACGGAGATCCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 snGluvalThrTyrLeuLeuProGlaAlaIleGlaValGlySerProThr
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Gaps: 8
Percent Identity: 38.393
          1460
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3246
          18.83
18.83
28.18
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106 1488 137 1576

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Chloroperoxidase; haloperoxidase; antifouling paint; preservative; halide; chloride; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......GATATAATATTCCCTGAAGTTAGTGAACTGGTCGAGGAGCT 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1699 ATTGCGATTGGAATCTTGGAGGAGCAGAGCTGACGTATGGCGAGAACTT 1748
                                                                                                                                         1132 CACGIGCIGAGICIGGIGACIGAAGIGGCIACGCGCGCGTIGAAGGCGGT 1181
                                                                                                                                                                                                                                                         1182 ACGGTATCAGAAGTTTAACATTCATCGTCGCCCTGCGGCCTGAGGCTACTG 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1317 CTCATCAATTCTGGATGACGTTGCTGAGAGCAATGAAAACAGAACAGGG 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 GlnValGlySerProThrHisProSerTyrProSerGlyHisAlaThrG1 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 IleThrvalargThrLeuHisGlnGluLeuMetThrPhealaGluGluAl 196
                                                                                     1 HisTyrPheArgLeuile ... GlyAlaAlaGluLeuAlaGlnArgAlaSe 16
                                                                                                                                                                                                    33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 rCysTyrGlnLysTrpGlnValHisArgPheAlaArgProGluAlaLeuG
                                                                                                                                                                                                                                                                                                                 1232 GIGGICIGATIATCGITAACAAGAAAICTITCCTIGCGGGTAGT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 snAsnGluVal.....ThrTyrLeuLeuProGlaAlaile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1417 GCCGAGGCCAGCCCATTCCATCCTATGGAAGTGGCCACGCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 . LeuAspArgGlyGlyGluCysPheProAsnProValPheProSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1517 AGATCGATAAGGTGTTCGAG........GTCGACACTGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AspGlyLeuGluLeuIleAsnPheGluGlyAlaCysLeuThrTyrGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1599 TGAATTGAACAAGCTCGCCGACAATGTTGCGATCGGGCGGAACATGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 lyileHisTyrArgPheAspGlyIleGlnGlyLeuLeuLeuGlyGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                             46 AlaAspPheAspIleSerLeuLeuGluAsnAspGluLeuLeuLysArg...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1367 CTGACGGGATTGTGAGCCCGGATAAATCATTTCTGTTGCCGATGGCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 mAsnGlyAlaPheAlaThrValLeuLysAlaLeuIleGly.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1552 GACAAGCTTGTGAAGTCGTCTTTCAAGGGAACT...CTCACTGTTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 yGluIleAsnLySLeuAlaValAsnValAlaPheGlyArgGlnMetLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1749 CTTCTTCAATTIGCCGAAATTCGACGGAACTACAATCCAGATT 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 aThrPheGluPheArgLeuPherhrGlyGluValileLysLeu 210
                                Align seg 1/1, to: V56021 from: 1 to: 1791
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ID T03875 standard; cDNA; 2088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haloperoxidase genes can be used for the recombinant production of the enzyme. The haloperoxidases of the invention are vanadium-dependent and have halide specificity of bronde and iodine:

Sequence 1791 BP; 390 A; 489 C; 435 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1998 (first entry)
Haloperoxidase, CP.BP02 encoding CDNA.
Haloperoxidase; enzyme; CP.BP01; CP.BP02; vanadium; hallde specificity; bromine; iodine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New haloperoxidase gene - and corresponding vector, transformed host cell and method of preparation Claim 2: Pages 15-18; 20pp; Japanese. This cDNA encodes a haloperoxidase enzyme. The haloperoxidase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codes a haloperoxidase enzyme. The haloperoxidase genes enzymes CP. BP01 and CP. BP02 are isolated from Corallina A host cell transformed with a vector containing the ase genes can be used for the recombinant production of the
                                .673 AGTICGAGICACTICIGCICGGIGAGGIGGGATIGGAAICTIGGAA 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATCCTGAAGGCGTTC....TTCGACTCCGGCATCGAGATC....G 1525
                                                                                                                                                                                                                                                                            1526 ATCAGGIGITCGAGGICGACAAGAIGAGGACAAGCITGIGAAGICGICI 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 GlnGluLeuMetThrPheAlaGluGluAlaThrPheGluPheArgLeuPh 203
HisProSerTyrProSerGlyHlsAlaThrGlnAsnGlyAlaPheAlaTh 106
                                                                                                               rValLeuLysAlaLeuIleGlyLeuAspArgGlyGlyGluCysPheProA 123
                                                                                                                                                                                                                        123 snProValPheProSerAsp.....AspGlyLeuGluLeuIleAsn 136
                                                                                                                                                                                                                                                                                                                                        PheGluGlyAlaCysLeuThrTyrGluGlyGluIleAsnLysLeuAlaVa 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 lAsnValAlaPheGlyArgGlnMetLeuGlyIleHisTyrArgPheAspG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 lylleGlnGlyLeuLeuLeuGlyGluThrIleThrValArgThrLeuHis 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag* a
/product* "Haloperoxidase, CP.BP02"
/note* "the stop codon is not indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 38.095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-151-189-2_COPY_441_676 x V56021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1773 IGATGGAACTACAATCCAGAIC 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 eThrGlyGluValileLysLeu 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID v56021 standard; cDNA; 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )6-MAR-1997; 070539.
16-MAR-1997; JP-070539.
5AKA ) DTSUKA PHARM CO LTD.
1817; 98-560733/48
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2.224
61.905
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06-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ulifera.
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SERVICE DE LA COMPANIA DEL COMPANIA DEL COMPANIA DE LA COMPANIA DE

W09527009-A1";

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822 TAACGGCGCGGGCACACGTACATAACGGCCGATATCGGCGACACGCAAT 87.
                                                                                                                                                                                                                  seq_name: N_Geneseq_36:T13683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.50
0.765
44.841
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2520 BP;
                                                                                                                                                                                                                                                                     seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENBANK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                         A CONR sequence (10387) codes for a chloroperoxidase (R82149) of Curvalaria inaequalis. The conk was obtd. by PCR using primers based on known sequences of the gene and by 5'RACE. The approtein encoded by the CDNA can be reactivated by addn. of vanadate. The cDNA can be reactivated by addn. of vanadate. The CDNA can be reactivated by addn. of vanadate. The CDNA can be the recompliant of vanadate into a vector for expression in procaryotic host cells. The recombinant chloroperoxidase is utilised in hailde (sep. chloride) analysis, or as an environmentally-friendly antifouling
                                                                                                                                                                                                                              Use of halo:peroxidase enzymes - in antifouling paints and methods for determining the halide concn. of liquids Example 3: Flg 6; 48pp; Erglish.
A CDNA sequence (T03875) codes for a chloroperoxidase (R82249) of
                                                                                                                                                         Van Schijndel JWPM, Vollenbroek EGM, Wever R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1289 CGACCTITGGCGGTGCTGTTCCAAATGGTGCGTCGGATACTACAACGG 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1339 CCGCGTAGGTACATGGAAGGACGACGACCGACAACATTGGCATCGATA 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1489 ATTGTTCGGCACTTCGACTCGGGCTGGGAACTCATGTTCGAAAACGCCAT . 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1562 ACTGGCGTTTCGATGCGGTCTCC......GCCCGCGACATTCTC 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1539 TICGCGTAIC.......................TICCICGGIGICC 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1600 ATTCCCACGACGACAAAGGACGTCTACGCTGTCGACAATGTCGCCCC 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               531 G; . 470 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 lathrGlnAsnGlyAlaPheAlaThrValLeuLysAlaLeulleGlyLeu 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eAsnLysLeuAlaValAsnValAlaPheGlyArgGlnMetLeuGlyIleH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 isTyrArgPheAspGlyIleGlnGlyLeuLeuLeuGlyGluThrIleThr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ValArgThrLeuHisGlnGluLeuMetThrPheAlaGluGluAlaThrPh 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 nalalleGlnValGlySerProThrHlsProSerTyrProSerGlyHisA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 IleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyrLeuLeuProG1 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .... AspArgGlyGlyGluCysPheProAsn.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1389 TGATGATCTCGGAGGAGCTCAACGGGTGAACCGCGACCTACGCCAGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....ProvalPheProSerAspAspGlyLeuGluLeulle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1439 ATGACCCCACGCCCCAATCGAAGACCAACCCGGTATCGTGCGCACCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ........AsnPheGlu...GlyAlaCysLeuThrTyrGluGlyGluIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 194
Gaps: 8
Percent Identity: 20.103.
            31-MAR-1994; EP-200893.
24-JUN-1994; U-001048.
24-SEE-) STICHTING SCHEIKUNDIG ONDERZOEK IN NEDER.
(TEWE.) STICHTING TECH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: T03875 from: 1 to: 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 C;
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US-09-151-189-2_COPY_441_676 x T03875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.000
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NL0123
                                                                                                                                                Dekker HL, Van Scr
WPI, 95-358602/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agent in ship pain
Sequence 2088 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                              WETENSCHAPPE
                                                                                                                                                                                                         P-PSDB
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Intertervals) and measure.

Claim 1; Page 90-186; 1223p; English.

T1356-731 show open reading frames 13, 20, 22-30, 32, 38, 41-46, 50-60, 62-63, 66, 66-79, 81-87, 91-92, 96-88, 101-103, 106-127, 129-130, 140-146, 148-150, 152 and 154 from a total of 154 ORFs identified in the Autopraphs californica nuclear polyhedrosis virus (AcRPO) clone 6. Each gene is numbered according to lits position in the virus genome beginning at the left end of the linear map; and irrespective of its orientation. The direction of transcription is relative to that some of the Polyhedrin gene. Of the 154 ORFs identified it was found that some of the ORFs (ORFs 27, 30, 32, 71, 86, 123, 126 and 127) are dispensable for virus replication in cell culture or insect larvae. These genes can be deleted from the genome to: (a) provide additional sites for insecting single or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       These genes can be deleted
as for inserting single or
aduce the size of the virus
83. Signal peptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tographs californica nublear polyhedrosis virus complete genome quence - useful in the prodm. of vectors for enhanced terologous protein expression, such as interleukin(s),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heterologous protein production;
                                                       1650 CGTGTTCCAGAACGTAGAGGACATTAGGTACACACCCAGGGGGACGCGTG 1699
198 eGluPheArg......LeuPheThrGlyGluValileLysL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               793 TCGTGCGTGGAA......GCGCATCCGTGCGCGTT 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 SerCysTyrGlnLysTrpGlnValH1sArgPheAlaArgProGluAlaLe 32
                                                                                                                                                                                                                                                                                                                                                                             nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 uGlyGlyThrLeuHisAsnThrIleAlaGlyAspLeuAspAlaAspPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               produ
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Gaps: 14
Percent Identity: 24.206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "corresponds to AcNPV 67884-70427"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s; and (b) t
designated
                                                                                                                                                                            1700 regacccccaeeccrcrrcccrarcecrer 1731
                                                                                                                     210 euPheGlnAspGlyThrPheSerIleAspGly 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1995; IEO578.
24-JUL-1994; GE-013420.
(NATU-) NATURAL ENVIRONMENT RES COUNCIL.
VYES M. Bishop D. Possee R;
PPI; 96-087670/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: T13683 from: 1 to: 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the genome to: (a) provide ac
multiple copies of foreign genes;
genome. The present sequence is de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
.US-09-151-189-2_COPY_441_676 x T13683
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                                                                                                                                                                                                                                                                                                                                   standard; DNA; 2520 BP.
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Possee R;

1 %															(uo)
49 spileSerLeuLeuGluAsnAspGluLeuLeuLysArgValAlaGluIle 65. :::::     :::    :::     872 ATTCAANTGTTGAATAATAACGAGTCACAACTGATAACGTGCATC 918	66 AsnalahlaGldAsnProAsnAsnGluValThITyrLeu	79LeuProGlnalalleGlnValGlySerProThrHisPro. 91	92	97HisalathrdlnAsnGlyalaPh 104 1057 GATAATTTCAAGTTATTTCCGACATCGAATGTGATGAATGA	104 ealathrvalleulysalaLeulleGlyLeuAspargGlyG 118	118 lyGluCysPhèProAsnProValPheProSexAspAspGlyLeuGluLeu 134	135 IleasnPheGluGlyAlaCysLeuThrTyrGluGlyGluIleasnLysLe 151	151 ualaValasnValalaPheGlyargGinMetLeuGlyIle 164	165HisTyrakgPheAspGlyIleGlnGlyLeuLeuGleuGlyGluThr 179	180 IlethrvalargthrLeuhisGlnGluLeumetthrPhealagluGlual 196	196 aThrPheGluPheArgLeu 202   111   11   119   119   1341 CATCTTGCTAATGCCTTTGGAAAGACAAAAGACCATCGGGC 1390	203PheThrGlyGluValIleLysLeuPheGlnAspGlyThrPhe 216	217 SerIle 218 ::::: 1441 GAIGIG 1446	seq_name: N_Geneseq_36:T13635	seq_documentation_block:  ID T1853 standard; DNA: 133894 BP.  AC T1855;  T1855;  T1855;  ACREA Girst entry)  DE ACREV genomic DNA clone 6.  NW Autographa californica nuclear polyhedrosis virus clone 6;  MY disruption; non-essential gene; heterologous protein product  NW expression vector; baculovirus; ss.  NW Autographa californica nuclear polyhedrosis virus clone 6:  PN WOSG01320-AZ.  PP 18-JAN-1996;  PR 04-JUN-1995; IN578.  PR 04-JUN-1995; RNSTRONMENT RES COUNCIL.

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open reading frames (ORFs 13, 20, 22-26, 28-30, 32, 38, 41-46, 50-60, 26-55, 66, 58-79, 31.87, 91-92, 96-98, 101-103, 106-1166, 129-130, 106-146, 148-150, 152 and 154 from a total of 154 ORFs identified by the patentees. See T13656-731 Expression vectors contg. the complete genomic sequence of AcRV, with the exception that at least one non-essential ORP is disrupted or replaced are useful for the synthesis of
                                                                                                                                                                                                                                       claims a polynucleotide selected from
                                                                                                                                                                                                                                                   129-130,
                                                                                                                                                                                                                                                                                                                                                                                                           40201 T;
                                                              witographa califoraica nuclear polyhedrosis virus complete genome
sequesce – useful la the prodn. of vectors for enhanced
severologous protein expression, such as interleukin(s).
                                                                                                                                                  closure; page 90-186; 122pp: Eaglish.
complete aucleotide sequence of the genome of clone 6 of
lovinus Autographa californica nuclear polyhedrosis virus
lovinus Autographa californica nuclear polyhedrosis virus
The sequence is taken from the Genbank
158. The pateat specification claims a polynucleotide sele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68876 ATGCATAGATTTACCCAAC......GGTACGGGCCAACATGTAT 68913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68729 TAACGCGCCGGACACACGTACATAACGCCCGATATGGCCGACACGCAAT 68778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68779 ATTICABARGITIGAATAATAACAGGG...TCACAACTGATAACGTGCATC 68825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68914 TCAAACACGTTGACGACGATATTTCGTACAACAGTGGCCAATTGGTGTGC 68963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69057 .....TTCCCAACTGAGGTGTTT.......GACGGCACC..... 69083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 lyGluCysPheproAsnProValpheProSerAspAspGlyLeuGluLeu 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .........HisAlaThrGlnAsnGlyAlaPh 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 eAlaThrValLeu......LysAlaLeuIleGlyLeuAspArgGlyG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 151 uAlaValAsnValAlaPheGlyArgGlnMetLeuGlyIle......164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 uGlyGlyThrLeuHisasnThrilealaGlyAspLeuAspAlaAspPheA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 spileSerLeuLeuGluAsaAspGluLeuLysArgValAlaGluIle 65
                                                                                                                                                                                                                                                                                                                                                                                                           27347 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 AsnAlaAlaGlnAsnProAsnAsnGluValThrTyrLeu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 .....LeuProGlnAlaIleGlaValGlySerProThrHisPro.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leagth: 252
Gaps: 14
Percent Identity: 24.206
                                                                                                                                                                                                                                                                                                                                                                                                             27151 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: T13635 from: 1 to: 133894
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US-09-151-189-2_COPY_441_676 x T13635
                                                                                                                                                                                                                                                                                                                                                                                                             39195 A;
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                                                                                                                                                                                                                                                                                                                                                                                         neterologous proteia
Sequence 133894 BP,
, Bishop 1
-087670/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
Percent Similarity:
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217 Serile 218

Percent Similarity:

Seguence

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5'-phosphate ester from the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl- or carbanyl-phosphoric acid, is reacted in its presence at µi 30 to 5.5. The PA can be used for the economic and efficient production of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and intermediates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Efficient production of nucleoside 5'-phosphate - by reaction of a nucleoside with a phosphoric acid donor in the presence of an acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xample 24; Pages 74-75; 95pp; Japanese.
The present sequence encodes the Serratia marcescens IAM 13540
acid phosphatase (AP), which can be used to produce a nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33304 .. TIAITITACICAAAAAACIIGGAAIAITGIITITAAGIIGGGCIAI 33350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33351 AATTGTAGCTTATAGAGTTTATGTTCGACTCATTATCCTTTGGATG 33400
                                                                                                                                                                                                                                                                                                                                                                                          33250 CCAAGCITICCAAGIGGICATACAACTITAGCATITACATIAGCAACAIC 33299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 lLeuLysAlaLeulleGlyLeuAspArgGlyGlyGlyCysPheProAsnP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 roValPheProSerAspAspGlyLeuGluLeuIleAsnPheGluGlyAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 CysLeuThrTyrGluGlyGluIleAsnLysLeu......AlaVe 153
                                                                                                                                                                                                                                                                                                                                         91 ProSerTyrProSerGlyHisAlaThrGlnAsnGlyAlaPheAlaThrVa 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.AUG-1997 (first entry)
Serratia marcescens IAM 13540 acid phosphatase DNA.
IAM 13540; acid phosphatase; production; nucleoside;
ester: condiment: phermaceutical; intermediate; ds.
Serratia marcescens.
                                                                                       Length: 91
Gaps: 2
Percent Identity: 25.275
                                                                                                                                                                                                                                                                            Align seg 1/1 to: V21209_11 from: 1 to: 110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a /*tag= //product= acid_phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mihara Y, Utagawa T, · Yamada H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33300 CITA .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 C;
                                                                                                                                                                                                 alignment_block:
US-09-151-189-2_COPY_441_676 x V21209_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 lyileGinGlyLeuLeuLeuGly 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seg_name: N_Geneseg_36:T45009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO CO INC
                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9637603-A1
                                                             alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nm base 1100001 (Methanococcus jannaschii circular LOCUS v21209 Accession v21209
halogenation and (with H2O2 and thiocyanate) as an antimicrobial. Sequence 2822 BP; 651 A; 808 C; 674 G; 689 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ........AsnPheGluGlyAlaCys...LeuThrTyrGluGlyGluIl 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1681 CCACCTTTGGCGGTGCTGTATTCCAGATGGTCCGCCGCTACTAGAACGGG 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1781 GATGATATCCGAGGAGCTCAACGGCGTGAACCGCGACCTGCGCCAGCCCT 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1831 ACGACCCGACTGCCCCCATCGAAGACCAACCAGGTATCGTCCGCACCCGC 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1881 ATCGTGCGCCACTTTGACTCAGCCTGGGAAATGATGTTCGAAAACGCCAT 1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1731 GGCGTAGGCACCTGGAAGGACGACCAGACAACATTGCCATTGACAT 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eAsnLysLeuAlaValAsnValAlaPheGlyArgGlnMetLeuGlylleH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......AlaLeuIleGlyLeuAspArgGlyGluCysPheP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 roAsnProValPheProSerAspAspGlyLeuGluLeuIle...... 135
                                                                                                                                                                                                                                                                                                                                                                                             65 IleasnalaalaGlnAsnProAsnAsnGluValThrTyrLeuLeuProGl 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 nAlaileGlnValGlySerProThrHisProSerTyrProSerGlyHiaA
                                                                                                                                          Length: 138
Gaps: 5
Percent 1dentity: 21.014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laThrGlnAsnGlyAlaPheAlaThrValLeuLys....
                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T51612 from: 1 to: 2822
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Continuetion (12 of 17) of V21209 from |
WP Sequence split into 17 fragments Low
WP Fragment Name Begin End
                                                                                                                                                                                                                                                     alignment_block: '
us-09-151-189-2_COPY_441_676 x T51612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seg_name: N_Geneseg_36:v21209_11
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                                                                                                                                              83.50
1.347
44.928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 isTyrArgPheAsp 169
                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136
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142 T;

198

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-phosphate esters. The method comprises reacting a nucleoside with hosphate donor at pH 3.0-5.5 in the presence of an acid phosphatese at hose been altered to increase its affinity for the nucleoside and/or increase its thermal stability, or in the presence of a microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that has been transformed with recombinant DNA containing a gene coding for such an acid phosphatase. Nucleoside 5' phosphates are useful as seasonings or pharmaceuticals or as intermediates for them note: this sequence appears to be claimed (claim 6), but as the claim protein is being claimed.
                                                                                                                                                                                                                                                                                                                          nucleoside with phosphate domor in presence of acid phosphatase
used as seasonings or pharmaceoutical intermediates
Example 24; Pages 47-48; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes an acid phosphatase enzyme. The specification describes a method for the preparation of nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 AACGCCTICGGCCTAGAAATAGCCCAACGGAAAACGCCGGGGCTGTTAA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 CCAAAATCACTATATGCGCATTCGCCCTTTGCGTTTTATAACGAAGCG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccrecreargaarccreageccceccarrrecceccaccecage 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 euileGlyteuAspArgGlyGlyGluCysPheProAsnProValPhePro 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ... AlaalaGlnAsnP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 roAsnAsnGluValThrTyrLeuLeuProGlnAlaileGlnValGlySer 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GlnArgAlaSerCysTyrGlnLbysTrpGlnValH18ArgPheAlaArgPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 GAMAATAGTGCGCAATACTCCGCGTGGCAAGCAGGCTTATGATGACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 oGluAlaLeuGly.GlyThrLquHisAsnThrIleAlaGlyAspLeuAap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 AlaAspPhe.....AspIleSerLeuLeuGluAsnAspGluLeuLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProThrHispro.....SerTyrPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '94 oSerGlyHlsAlaThrGlnAsnGlyAlaPheAlaThrValLeuLysAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 ACGTIGCCGGGACGCC......GITGCCGCCGCATTITCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 210 Gaps: 10 Percent Identity: 23.333
                                                                                                                                                                                                                                                                                                        nucleoside 5'-phosphates comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allgn seg 1/1 to: V43062 from: 1 to: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 C;
                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 sArgValAlaGluIleAsn.....
                                                                                                                                                                           (AJIN ) AJINOMOTO CO INC.
ASBRO Y, MINBLE Y, Utagawa T, Yamada
WPI; 98-416010/36
Locatlon/Qualifiers
1. .735
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US-09-151-189-2_COPY_441_676 x V43062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.50
0:823
47.143
                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratlo:
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                                                                                                                                                                                                                                                                              W71033
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                                                                                                                                                 18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                          20-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
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DNA encoding an acid phosphatase enzyme.
Acid phosphatase; preparation; nucleoside 5'-phosphate eater;
Seasoning; intermediate; ds.
Serratia ficaria
                                                                                                                                                                                                                                                                                                                    198 GAAAATAGTGCGCAATACTCCGCGTGGCAAGCAGGCTTATGATGACGCCC 247
                                                                                                                                                                                                                                                                                                                                                                                                        .....AACCCC..... 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 rGluGlyGluIleAsnLysLeuAlaValAsnValAlaPheGlyArgGlnM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 GCTGGTGAAAATGCGTGAAGACGCCGGCGATTTGGCGACCCGCAGGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 CCAAAATCACTATATGCGCATTCGCCCTTTGCGTTTTATAACGAAGCG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 ACCTGCCGACCGGACGAAGAAAGCACCCTGTCGAAGAACGGTTCTTACCC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eulleglyLeuAspArgGlyGluCysPheProAspProValPhePro 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerAapAspGlyLeuGluLeuIleAsnPheGluGlyAlaCysLeuThrTy 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GCCAG 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 CCAGGGTGAAATCCTGCAGCGCGGCTATGATATGGGCCAAAGCCGGGTTA. 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGCGGTTATCACTGGCAAAGCGAC...GTGACTGCGGCGCCGATGGCG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 GluThrlleThrValArgThrLeuRisGlnGluLeuMetThrPheAla. 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643 GCGTCGGCCATGGTGGCGCGTTGCATGCCGAA...CCCACCTTCGCCGC 689
                                                                                                                                                                                                                                                                                                                                                                29 oGlualaLeuGly.GlyThrLeuHlaAanThrIlaAlaGlyAapLeuAsp 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSerGlyHisAlaThrGlnAanGlyAlaPheAlaThrValLeuLySAlaL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                  13 GlnArgAlaSerCysTyrGlnLysTrpGlnValBiaArgPheAlaArgPr 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 roAsnAsnGluValThrTyrLeuLeuProGlnAlaIleGlnValGlySer 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sArgvalAlaGluIlaAsn........AlaAlaGlnAsnp 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProThrHispro.....serryrPr 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 AlaAspPhe .... AspIleSerLeuLeuGluAsnAspGluLeuLeuLy
                                     Length: 210 Gaps: 10 Percent Identity: 23.333
                                                                                                                                                                                                              to: T45009 from: 1 to: 735
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                                                                                                                                  alignment_block:
US-09-151-189-2_COPY_441_676 x T45009
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ID V43062 standard; DNA; 735 BP.
                                                                0.823
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                                        81.50
                                        Quality:
                                                                                 Percent Similarity:
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482 111

ON NEW YORK

Thu May 18 22:21:30 2000

Claim 1; Page 1230-1232; 1409pp: Engiish

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Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagaostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae; S. paeumoniae; geaome; diagnosis; sssay; computer readable medium; vaccine; pharmaceutical composition; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1221 TCGACTTCTTCCAGTCGCCCAGTTTTTGCCCCAACCCGCCTGGCCTGGAA 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1271 GCCCTCASCCCAACACCAGCTGCCGCCACTTC......CC 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1034 GAGCTGAGCATCGCCGAGGGCCAGGAAGTACTATTTGGGGTCTTTGTGAC 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1134 TCCCCATTGACCTGCTGGACACACTAATTGATGAGGGGTGTGGAGCGCTGT 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1306 TCTGCTGGTCAGTAGCAGCTTCTCACGTGTGGACCTA......1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 nGlyAlaPheAlaThrValLeuLysAlaLeuIleGlyLeuAspArgGlyG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 lyGluCysPheProAsnProValPhe. .. ProSerAspAspGlyLeuGlu 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 LeuileAsnPhéGluGlyAlaCysLeuThrTyrGluGlyGluifeAsnLy 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 sLeuAlaValAsnValAlaPheGlyArgGinMetLeuGlyIleHisTyrA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 rgPheAspGlyIleGlnGlyLeuLeuLeuGlyGluThrIleThrVaiArg 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 ThrLeuKisGluGluLeuMetThrPheAlaGluGluAlaThrPheGluPh 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 eArgleuPheThrGiyGiuVailieLys.....LeuPheGlnA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1435 GCGTATCCTGCAGGTGGAGCTGGTCAGGTCACTAAACTACTTGCTGTATG 1484
                                                                                        49 AspileSerIeuLeuGluAsnAspGluLeuLeuLysArgVal..... 62
                                                                                                                                                                                                                                  63 .... AlaGluIleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyr. 77
                                                                                                                                                                                                                                                                                                                                                                             78 ......LeuLeuProGlnAlaileGlnValGly..... 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae genome fragment SEQ ID NO:220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
Sarash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
Align seg 1/1 to: V72100 from: 1 to: 4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1485 IGICCAACTICICACIG...GGIGAC 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 spGlyThrPheSerIleAspGlyAsp 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID V52353 standard; DNA: 4692 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_neme: N_Geneseq_36:V52353 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reptococcus pneumoniae
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This sequence encodes a novel humae macrophage stimulating protein, MSP, receptor (the RON receptor) which is used in a method for the prophylactic treatment of a tumour derived from acaroendocrine cells (NEC) by administration of this MSP to a subject at risk, sufficient to induce apoptosis of ROC expressing a RON receptor (the receptor for MSP). The method is especially used to treat or prevent small cell lung cardinoma and apoptosis of RON-expressing cells may be iaduced in vivo or in vitto. Screening NEC from a subject for susceptibility to MSP-induced apoptosis is used to identify patients who will benefit from treatment with the MSP protein. MSP is already known for treating pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infections, for stimulating thrombocyte production and megakaryocyte maturation (for treating thrombocytopaenia) and for stimulating growth of cells (particularly hepatocytes) 1384 C; 1309 G; 986 T; Sequence 4541 Bp; 662 A; 1384 C; 1309 G; 986 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSP; macrophage stimulating protein; apoptosis; human; treatment; neuroendocrise cell; RoN receptor; small cell lung cardinoma; tumour; pathogen infection; thrombocyte production; megakaryocyte maturation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating tumours derived from neuroendocrine cells with macrophage stimulating proteia - or its nucleic acid, also for preventing development of these tumours, specifically small cell lung carcinoma bisclosure; Page 73 800: 100pp; English.
                128 SerAspAspGiyLeuGluLeuIleAsnPheGluGiyAlaCysLeuThrTy 144
                                                                                        541 ......GCCAG 545
                                                                                                                                                               144 rGluGlyGluIleAsnLysLeuAlaValAsnValAlaPheGlyArgGlnM 161
                                                                                                                                                                                                                                  546 GCAGGGTGAAATCCTGCAGCGCGCTATGATATGGGCCAAAGCCGGGTTA 595
                                                                                                                                                                                                                                                                                                                                                                             596 TCTGCGGTTATCACTGGCAAAGCGAC...GTGACTGCGGCGCGGATGGCG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                178 GluThrileThrVaiArgThrLeuHisGlnGluLeuMetThrPheAla.. 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   643 GCGTCGCCATGGTGCCGCTTTGCATGCCGAA...CCCACCTTCGCCGC 689
                                                                                                                                                                                                                                                                                                         161 etLeuGlylleHisTyrArgPheAspGlylleGlnGiyLeuLeuGly 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 47.917 Percent Identity: 25.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "RON receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 .....GluGluAlaThrPheGluPhe 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          690 CCAGGTGCAAAGGGCAAAGACGAATTC 717
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/product- "RON recep-
/note- "MSP receptor
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US-09-151-189-2_COPX_441_676 x V72100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2100 standard; cDNA; 4541 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1999 (first entry)
Human RON receptor CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq_name: N_Geneseq_36:V72100
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WPI: 99-059877/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -JUN-1998; U11573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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Ratio:
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the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded on 1t. or a representative fragment or a sequences at least 5% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEO ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in STO ID NO: 1 that by this dentifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating in diagnosis kits and assays, and pharmaceutical invention describes a computer readable medium which has de sequences SEQ ID NO:1 to 391 (V52134 to V52524) recor . Products from the present 1480 TCCAGAAGATACCAAGGGTCTGTTATGCAAAGCCTTTCTGAACGTAAAG 1431 1430 GTGAANTGTTGGAIATGAITTCAACTGGTAATGGTCAAACTCGTTTGGTC 1381 1380 TICCITGITGIGGCGCGCGTGGTTGGATACTCACTGAGTTCTTATC 1331 1280 CATTGATTCCAGGGGAAATTGGTGGACGTGACCGTGGTGCCCTTGTTTCT 1231 1230 ATCGAIGCIGGIAAGGCIACAACTIACICAAICAIGICIAIGGAAGAACG 1181 1530 GAAATCGACGGTATTAAATGTGAACCATTTGAACGTGTACAAATCGACAC 1481 1580 GTCGTGAGGGCTATGAACTTCAAGTATGTCGTCCAGAAGTTATCGTAAA 1531 1330 AATGACTCGTGGTTACGGTATCATGAACCATACCTTCGACCAATACTTGC 1281 rTyrProSerGlyHisAlaThrGlnAsnGlyAlaPheAlaThrVaiLeuL 109 ys.....AlabeulleGly 113 114 LeuAspArgGly......117 85 118 .GlyGluCysPheProAsnProVaiPheProSerAspAspGlyLeuGluL 134 \* 44 uAspAlaAspPheAspIleSerLeuLeuGluAsn... AspGluLeuLeuL 60 60 ysArgVafAiaGluIleAsnAlaAiaGlnAsnProAsnAsnGluValThr 76 7 35 ThrLeu.....HisAsnThrlieAlaGlyAspLe 77 TyrLeuLeuProGlnAlalleGlnValGlySerProThrHis....ProSe 17 CysTyrGlnLysTrpGlnVal.His...... 820 G; to reverse of: V52353 from: 1 to: 4692 Gaps: 12 Percent Identity: 18.952 Length: 1008 C: alignment\_block: US-09-151-189-2\_COPY\_441\_676 x V52353/rev pneumoniae genome 1429 81.00 0.711 45.968 ragments of the S. pneumcran to the compositions and vaccines sequence 4692 Bp: 142 alignment\_scores:
 Ouality:
 Ratio:
 Percent Similarity: invention car compositions Align seg 1/1 Sequence 601. 2 88888888888888888888888888888

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The present Invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO: 1 to 391 (V5234 to V5524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences of the SEQ ID NO: 1 to 391. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO: 1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO: 1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g fragments of the or expression modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ication primers derived from the snow to prime the amplification and as. The computer readable medium can be for identifying fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism, amplifying nucleic acid molecules whose nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae genome fragment SEQ ID NO:46. STreptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds. Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present
                                                                                                                                               1148 TI.....TATGAAGGAATGATCATCGGTGAAAACTCTCGTGAAAATGAC 1105
                                                                                                                                                                                                                                                                                                                                               1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1071 ....accaacticgticactactaaggaccaaacactgtitititities
                                                                                                                                                                                                                                                  151 LeualayalasnyalalaphqflyargGlnMetLeuGlyIleHisTyrar 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1025 CG.....CCTCGTATCTTGACACTTGAAGAGTCTCTTGACTTCTTGAAC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in diagnosis kits and assays, and
                                                                               134 eulieAsnPheGluGlyAlaCysLeuThrTyrGluGlyGluileAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                          167 gPheAspGlyIleGlnGlyLeuLeuGlyGluThrIleThrValArgI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 hrleufisgingluleuMetThrPheAlaGluGluAlaThrPhe.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1997; U19588.
31-OCT-1996; US-029960.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Chol GH, Dillon PJ, Dougherty BA, Fannon M,
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Products from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             981 GACGATGAGTACATGGAAGTAACGCCTGAGTCTATCCGTTTG 940
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1180 IGGIACGAICTITGICAACCCA........
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DE V52179; standard; DNA; 7577 BP.

DE 23-OCT-1998 (first entry)

DE Streptococcus pneumoniae; S. pneumoniae;

NS Streptococcus pneumoniae; S. pneumoniae;

NO9818931-A2.

PP 07-MAY-1998.

PP 07-MAY-1998.

PP 07-MAY-1998.

PP 10-COT-1996; US-029960.

PR 10-MA-1996; US-029960.

CC 1996; US-0296; US-029960.

CC 1996; US-0296; US-029960.

CC 1996; US-0296; US-029960.

CC 1996; US-0296; US-0276; US-027
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203

Length: Gaps:

Ouality: ... Ratlo:

alignment\_scores

Length: 226 Gaps: . 15 Percent Identity: 23.009

to: 12019

from: 1

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The present sequence encodes Alcaligenes sp. proteins PoxR, PoxB, PoxC, The proteins are useful in the fields of petroleum pUrification, chemical industry and drug industry related to the synthesis, conversion and decomposition of sequence 12019 BP; 2015 A; 4104 C; 4151 G: 1747 T:
                                                                                                                                    W98976, W98977, W98978.

New encoding an aromatic cpd. oxidative decompsn. enzyme - useful in the fields of petroleum purification, chemical and drug industries claim it Page 7-19; 35pp, Japanese.
                                                                                                                  W98969, W98970, W98971, W98972, W98973, W98974, W98975,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9980 CAAGCTCGGCTGC...CAGACCGGCGACCTGAATCCGGACCCC...TGGC 10023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10024 ccaccaccrecececarececesconscentices...cacrecers 10070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10112 TGACGTGCTGCGCTTCTCGCTGCCCGAGGTGGTGGCGGGGGGCCGGAGC 10161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10071 CTGTACGGCGACGACCTCAACGCC.....ACGGTCAAGCTGTTCCG 10111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10162 GGATGGTGATCGCCGCCTTCCTGACTGGACAAGGCGCCACGACATC 10211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9722 CCGCGTCTACCTGAAGGCCTGGGACGAGGACGACCAT.....9758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9759 ......cacagcgrggrgcrgcgcgagccgaCagcccg 9791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3792 GGCATGCACTACATGGGCTTCCGCGTCGACAGCGATGCCACGCTGGAGCG 9841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9942 CCGACCGGCCATGCCATCGAG.....CTGTTCGCGGAC.....AAGGA 9979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9892 TCCCCGCCGCGAGCACCTGCGCACCGGCCGCCTTCCGCTTCACCATT 9941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 174 ..LeuLeuLeuGlyGluThrIleThrValArgThrLeuHisGlnGluLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9842 GCTGGCGGCCGAAGTGCCCGCCAGGGCTGGCGCAGGACTGCGCCTGGA 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 ProSerGlyHisAlaThrGlnAsnGlyAlaPheAlaThrValLeuLysAl 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roSerAsp...AspGlyLeuGluLeuIleAsnPheGluGlyAlaCysLeu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThriyrGluGlyGluIleAsnLySLeuAlaValAsnValAlaPheGlyAr 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 aLeulleGlyLeuAspArgGlyGlyGluCysPheProAsnProvalPheP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 laLeuGlyGlyThrLeuKisAsnThrIleAlaGlyAspLeuAspAla... 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 gvalalaGluileAsnalaAlaGlnAsnProAsnAsnGluValThrTyrt 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 .... CysTyrGlnLys...TrpGlnValHisArgPheAlaArgProGluA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HisTyrPheArgLeuileGlyAlaAlaGluLeuAlaGlnArgAlaSer...
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US-09-151-189-2_COPY_441_676 x X18867
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0.694
51.327
JP-200625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
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Claim 1, Page
The present a
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    25-JUL-1997
(TOFU ) TOW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159
             Alcaligenes Sp. Pox Proteins R, A, B, C, D, E, F, G, H and I coding DNA. Alcaligenes Sp. Pox Proteins R, A) and PoxI; Alcaligenes; PoxI; PoxI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5222 AAGAGGAANTITATGAGTATTAAA...CTAATTGCCGTTGATATCGACGG 5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5369 CCTATCGCAGGCGTTGCCAAACTTCTAGACGACTTGCAGTTGAGAGACGA 5418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5319 TCCAAGATGCCAAAGAAGCTGGTGTCAAAGTCGTGATTGCAACTGGCCGC 5368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5469 CAGGACATGAGATTATCAGCGAATCCTTGACTTATGAGGATTATCTAGAT 5518
                                                                                                                                                                                                                                                                                                                                     5072 ATCGTCCAATCCCTTGCTGGCAGTCGCACGGAGATAATCGCTTTTATTT 5121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5122 TCCAAAAGAAATGTTGGACCAAACAGCATCTTTGCAAGCATTACCCAGC 5171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5269 AACCCITGICAACAGCCAAAAGGAAATCACTCCTGAAGIITITICIGCCA 5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5419 GGGGACTATGTGGTAACCTTCAACGTGCCCTTGTCCAAGAACTGCTA 5468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5172 AATTTTTACACTTGATTGAGAACGATCATTTTACCCCAAATAAAACTAG 522]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 .....ValPheProSerAspAspGlyLeuGluLeuIleAsnPheGluGl 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 ......LeuAlaValAsnValAlaPheGlyArg 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 GlnMetLeuGlyIleHlsTyrArgPheAspGlyIleGln......172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......GlyLeuLeuGlyGluThrIleT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 rProSerGlyHisAlaThrGlnAsnGlyAlaPheAlaThrValLeuLySA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 laLeuIleGlyLeuAspArgGlyGlyGluCysPheProAsnPro..... 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 lulleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyrLeuLeuPro 80
                                                                                                                                                                                                                                                                   37 HisAsnThrileAlaGlyAspLeuAspAlaAspPheAspIleSerLeuLe 53
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                                                                                                                                                                                                                                                                                                                                                                                                                         53 uGluAsnAsp.....GluLeuLeuLysArgValAlaG
    Percent Identity: 20.690
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                                                                      alignment_block:
US-09-151-189-2_COPY_441_676 x V52179
                                                                                                                                                                                        to: V52179 from: 1
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ID X18867 standard: DNA; 12019 BP.
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    47.783
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25-JUL-1997; 200625.
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Percent Similarity:
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..........GCGCATGCCTTTAGTTTCCCT 192

.....TGCTATTCTAAC .....G

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283 ...GGTGCTATTATTTTACTTTTTTGGATTTTTTAATGGCGTATGATAG 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 GluGlyGluIleAsnLysLeu.....AlaValAsnValAlaPheGlyAr 159
126 TITAGIGGGGGGCCCACGGCCTGTAACCAAIGGCGAAITGGITITI ... 171
                                                                                                                                                                                                                                    95 SerclyHisAlaThrGlnAsnGlyAlaPheAlaThrValLeuLySAlaLe lll
                                                                                                                                                                                                                                                                                                                                                                                                          128 erAspAspGlyLeuGluLeuIleAsnPheGluGlyAlaCysLeuThrTyr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 GGTTTATTTAGGGGTGCATTACCCTAGCGATGTTTTAGGAGGGTTTTTAT 379
                                                              64 ulleAsnAlaAlaGlnAsnPro.....AsnAsnGluValThrTyrLeuL 79
                                                                                                                                                                                                                                                                            193 AGCGGCATGCTTTAGCTTCAGCGCTTTTTTACGGCTCTTTGGCGTTGTT
                                                                                                                                                  79 euProGlnAlalleGlnValGlySerProThrHisPro...SerTyrPro
                                                                                                                                                                                                                                                                                                                           111 ulleGlyLeuAspArgGlyGlyGluCysPheProAsnProValPheProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 CAACCATCGCATTAAAACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 euGly 177
                                                                                                                                                                                                                                                                                                                                                                     243 GTTA.....
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d for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to treat or prevent H. pylori
lori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein of unspecified function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ri polypeptide binding compounds
fe cycle activators or interest
                                                                   10212 GCCTTCATCCGCCACGCGGAGAACCGCTTCCATCACGCTTCGTTCCA 10261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particular regions can be isolated from H. pylori
                           190 .....MetThrPheAlaGluGluAlaThrPheGluPheArgLeuPheTh 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 T;
                                                                                                                                                                                                                                                                                                                                                    treatment; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determined the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the predicted
                                                                                                                                                                                                                                                                                                                                               Tytoplasmic; vaccine; prevention: treatment; infection identification; binding compound; bacteria; life cycle inhibitor; duodenal ulcer disease; chronic gastritis;
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                                                                                                                                        10262 GCTCGACACTGGAGCGAGGTGCTGAAG 10289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i. pylori-specif.
                                                                                                             204 r....GlyGluvalIleLys 209
                                                                                                                                                                                                                                                                                                                                                                                                                                      Acation/Qualiflers
                                                                                                                                                                                                                                           seq_documentation_block:
ID v24666 standard; DNA: 453 BP.
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ORF 06ce10808orf2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be
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1.246
46.667
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                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylor
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Ouality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                            -JUL-1998
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48 PheaspileSerLeuLeuGluAsnAspGluLeuLeuLysArgValAlaGl 64

Align seg 1/1 to: V24666 from: 1 to: 453

alignment\_block: US-09-151-189-2\_COPY\_441\_676 x V24666

Gaps: Percent Identity: 26.66

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    No. 58663930 No. 5866393disk of No. 5866393th America, Inc.
Social Lexington Avenue, Suite 6400

                 69.50 114.65 63.13 69.50 114.65 63.13 69.50 114.65 63.13
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fugisang, Claus
APPLICANT: Halkter, Torben
APPLICANT: Oxenboll, Karen M.
APPLICANT: Berka, Randy M.
APPLICANT: Derka, Randy M.
APPLICANT: BINYBRIDIN: Raloperoxidases from Curvularia
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 lleAsnAlaAlaGlnAsnPrOAsnAsnGluValThrTyrLeuLeuProGl 81
                                                                                                                                                             seg_name: /cgn2_6/ptodata/1/ina/5C_COMB.seg:US-08-679-405-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION WOMBER: 05/08/679,405 CLAURE DATE: 04/09 9, 1996 CLAURE DATE: 04/04 9, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 21.014
             /cgn2_6/ptodata/l/lna/5C_COMB.seq:US-08-694-865-5 + 
/cgn2_6/ptodata/l/lna/5D_COMB.seq:US-08-878-748-5 + 
/cgn2_6/ptodata/l/lna/5D_COMB.seq:US-08-535-837-1 + 
/cgn2_6/ptodata/l/lna/6_COMB.seq:US-08-124-491-5 +
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US-09-151-189-2_COPY_441_676 x US-08-679-405-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIPICATION: 43 5, 23 9 CLASSIPICATION: 43 5, 23 9 CLASSIPICATION NUMBER: 60/001,194 PILING DATE: 50/101 PILING DATE: 50/101 PAPLICATION NUMBER: 08/603.534 FILING DATE: February 21, 1996 ATTONREY ADMINISTRATION: NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                E: Floppy disk
1BM PC compatible
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MOLECULE TYPE: DNA (genomic)
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TELECOMMUNICATION INFORMATION
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TELEPAX: (212) 878-9555
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2822 base pairs
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy d
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-WODEL-frame-p2n.model -DBV-x1p
-W-OG912_1/OSPC_appo_1/YG015189/runat_15052000_082513_1631/app_query.fasta.1
-Woden2_1/OSPC_appo_1/YG015189/runat_15052000_082513_1631/app_query.fasta.1
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-XGAPEXT=0.000 -GGARPOP=4.500 -GARPEXT=0.000 -XGAPOP=10.000
-YGAPEXT=0.500 -FELOPE-6.000 -FGAPEXT=7.000 -XGAPOP=10.000
-YGAPEXT=0.500 -FELOPE-6.000 -FGAPEXT=7.000 -XGAPEXT=0
-WARTX-D10sum62 -TRANS-human40.cdi -L15T=45 -DGCALIGN=200
-THR_SCORE-PCT -MINGN=15 -WODE-LOCAL -OUTFAT-Pfs -NORM-ext
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OM of: US-09-151-189-2_COPY_441_676 to: Issued_Patents_NA:* out_format : pfs
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                                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 compugen Ltd.
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Ptodata/1/ina/5A_COMB.seq:U5-07-908-253-1

Ptodata/1/ina/5B_COMB.seq:US-08-455-970A-1

ptodata/1/ina/5B_COMB.seq:US-08-455-970A-1

ptodata/1/ina/5B_COMB.seq:US-08-387-156-5
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Query: US-09-151-189-2_COPY_441_676
Query: US-09-151-189-2_COPY_441_676
Database: Issued_Patents_NA:*
Database agequences: 226296
Database length: 63486255
Search time (sec): 41.480000
                                                             Date: May 17, 2000 10:57 AM
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1831 ACGACCGACTGCCCCATCGAACACCAACGGTATCGTCCGCACCCGC 1880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 21.014
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US-09-151-189-2_COPY_441_676 x US-08-842-799-1
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ENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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   Quality:
   Ratio:
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CHO
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1831 ACGACCCGACTCCCATCGAAGACCAACCAGGTATCGTCCGCACCCGC 1880
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                                                   81 nAlaileGlnValGlySerProThrHisProSerTyrProS
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1881 ATCGTGCGCCACTTGACTCAGCTGGGAAATGATGTTCGAAAACGCCAT 1930
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                                                                                                        136 ......AsnPheGluGlyAlaCys...LeuThrTyrGluGlyGluIl
                        122 roAsnProValPheProSerAspAspGlyLeuGluLeulle
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05-May-1995
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Verruculosa and Nucleic Acids Encoding Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 nAlalleGlnValGlySerProThrHisProSerTyrProSerGlyHisA
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                                                            lovo Nordisk of North America, Inc.
Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                     atentin Release #1.0, Version #1
ATION DATA:
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US-09-151-189-2_COPY_441_676 x PCT-US96-11458-1
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4-JUL-1995
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                                                                                                                                                                                                                                                                                                                               -JUL-1996
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477..2276
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EDIUM TYPE: Floppy
TITLE OF INVENTION:
                                                                                                   New York
New York
U.S.A.
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Percent Similarity:
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THOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
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                                                                                                                                                                                                              JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
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US-09-151-189-2_COPT_441_676 x US-08-975-698A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ION NUMBER: US/08/975,698
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IAM 13540
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                                                                                                                                                                                                                                                                                                                                                                                                 IBM. PC CO
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STRANDEDNESS
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US-08-975-698A-27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ......GTTGCCGCCGCATTTTCC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 ACCIGCCGACCGGACGAAGAAAGCACCCIGTCGAAGAACGGTTCTTACCC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 oSerGlyHlsAlaThrGlnAsnGlyAlaPheAlaThrValLeuLysAlaL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 TICCGGCCAIACCACCAICGGCIGGCGACCGCGCIGGIGCTGGCAAA 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 rGluGlyGluIleAsnLySLeuAlaValAsnValAlaPheGlyArgGlnM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 GCAGGGTGAAATCCTGCAGCGCGGTATGATATGGGCCAAAGCCGGGTTA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 etLeuGlylleHisTyrArgPheAspGlylleGlnGlyLeuLeuLeuGly 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GluThrIleThrValArgThrLeuHisGlnGluLeuMetThrPheAla. 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 euileGlyLeuAspArgGlyGlyGluCysPheProAsnProValPhePro 127
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                                                                                                                                                                                                                                                                                                                                                                        13 GlnArgAlaSerCysTyrGlnLysTrpGlnValHisArgPheAlaArgPr 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 oGluAlaLeuGly.GlyThrLeuHisAsnThrlleAlaGlyAspLeuAsp 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 CCAAAAATCACTATATGCGCATTCGCCCCTTTGCGTTTTATAACGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 AACGCCTTCGGCCTAGAATAGCCCAACGGAAAACGCCGGAGCTGTTTAA
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                                                                                                                                                             Percent Identity: 23.333
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US-09-151-189-2_COPY_441_676 x US-08-750-145A-23
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; LOCATION:
US-08-750-145A-23
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LENGTH: 1188 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double	3Y: 11ne TYPE: I ICAL: NO	ORGANISM: Vibrio cholerae CRGANISM: Vibrio cholerae STRAIN: Classical 395 ' IMMEDIATE SOURCE:	; CLONE: OrtU US-08-624-601-3	alignment_scores:	alignment_block: US-09-151-189-2_COPY_441_676 x US-08-624-601-3	Align seg 1/1 to: US-08-624-601-3 from: 1 to: 1188  32 LeuGlyGlyThrLeuHisAsnThrlleAlaGlyAspLeuAspAlaAspPh 48	AIGGCTICGACICICAAICAIGICAGIGGICAGGIGCCCACICICA  eAsplleSerLeuLeuGluAsnAspGluLeuLysA				93 yrProSerGlyHlsAlaThrGlnAsnGlyAlaPheAlaThrValLeuLys 109	110 AlaLeulleGlyLeuAspargGlyGlyGlyGluCysPhe121	122ProAsnProValPheProSerAspAspGlyLeuGluLeuI 135	135 leAsnPheGluGlyAlaCysLeuThrTyrGluGlyGluIleAsnLysLeu 151 	152	159 gGlDHetLeuGlylleH1sTyrArgPhe	169AspGlylleGlnGlyLeuLeuLeuGlyGlvThrIle 180 :::    :::    ::::::::     953 AGTTAGAAAGGCTCAGCAGAATTTAAAGCAGATGATCAACGATAAAATC 1002
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71 roAshAsnGluValThrTyrLeuLeuProGlnAlaIleGlnValGlySer 87 :::	88 PIOTATHISPIO SETTYPP 94 1::111 433 ACCIGCGACGACGACGAAGAAGCACCCIGTCGAAGAACGCTTCTTACCC 482	94 oSerGlyHlsalaThrGloAsnGlyAlaPheAlaThrValLeuLysalaL 111 	111 eulleGlyLeuAspArgGlyGlyGluCy8PheProAsnProValPhePro 127	128 SerAspAspGlyLeuGluLeuIleAsnPheGluGlyAlaCysLeuThrTy 144 ::: 541	144 IGLUGIYGLUILeAsnLysLeuAlaValAsnValAlaPheGIyArgGlnM 161 :::          :: :::::::: :::		178 GluthrllethrValArgthrLeuHisGlnGluLeuMetthrPheAla 193 :::	194GludlualathrPheGluPhe 200 690 ccagcrGcalaaGGCCaalgacGaarrc 717	.name: /cgn2_6/ptodata/l/ina/5C_COMB.seq:US-08-624-601-3 documentation_block: quence 3, Application US/08624601	nnes B. Vyron M.	TITLE OF INVENTION: VIDELA CROLEFAGE OL (CVDIII) and non-OI TITLE OF INVENTION: (CVDIIZ and CVDIIZRM) serogroup vaccing TITLE OF INVENTION: of making same and products thereof CORDERSONMENCE AND ADDRESS 16	CANGRAGNIENCE AUDINESS: ADDRESSEE: Spencer & Frank STREET: 1100 New York Ave. N.W. Suite 300 East GTTY: Washington	COUNTRY: USA ZIP: 20005 AUDPITER FRADABLE FORM:	MEDION ILE: FIGHY UISA COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0; Version #1.30	APPLICATION UNDER: US/08/624,601 FILING DATE: 08-APR-1996 CLASSIFICATION: 424 APPLICATION: AINCHARA	ALIONELLY ACENT INFORMATION: NAME: Schneller Dr., John W. REGISTRATION NUMBER: 26,031 REFERENCE/DOCKET NUMBER: BAMC20019P2	TELEFAX: (202)414-4000 TELEFAX: (202)414-4000 TELEFAX: (202)414-4040  INPORATION FOR SEQ 1D NO: 3: SEQUENCE CHARACTERISTICS:

OBZANTEM. Vibrio cholerae	CLASSICAL CDS	FEATURE:  NAME/KER:  NAME/KER:  CONTROL  CONTROL			Percent Similarity: 47.881 Percent Identity: 23.729	alignment_block: US-09-151-189-2_COPY_441_676 x US-07-931-943-1	Align seg 1/1 to: US-07-931-943-1 'from: 1 to: 2912	32 LeuglyddyrhriauHisAsnThrileAladlyAsplauAspPh 48	1478 AIGGCITCCACICTCAAICAIGICAGICAGGICAGGICACACICTCA 1524	eAspIleSerLeuLeuGluAsnAspGluLeuLeuLysA	1525 AGATATGGTTCAGCTCAATACGAAGTTTCACGCGGACCGTGTTCTTGAAA 1574	rgValAlaGluIleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyr'	AAGTGAACGCAATCAAC AATCGATTGAATGGGCAGATAAACTAT	LeuLeuProGlnAlaIle	CTIGAAGAAGITCGCAICGATGIAIGGGAIACACAACGGGAGGICAGAAA	84		ACCAAAGTAAGATGCT GTGCTTCGG	AlaLeuIleGlyLeuAspArgGlyGlyGluCysPhe	1745 GCGAITGAIGAGCTIAAAGAITCACICGGIGGGGITGICGITCCGCCIAA 1794	122ProAsnProValPheProSerAspAspGlyLeuGluLeuI 135	CACGCCACC	135 leAsnPheGluGlyAlaCysLeuThrTyrGluGlyGluIleAsnLysLeu 151		GAGACGATICACAGCAACIOGACACCAIGAACACGGCGCIAI	gGinWetLeuGlylleHisTyrArgPhe	CIGIAGIAACCCIGCICGCIGICAGIIICCGAIACGCGAGGCCGAGACCG	169Aspolylledinglyleuleuleudigluluhrile 180   1986 agttagaaacggctcagcagaatttaaaggcagaacgaatgaacaacaataaaac 2035	181 ThrValargThrLeuMisGlDGluLe 189 	the second secon
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	CAAAGGCTCG	TTACAACCT		SA_COMB.se			, Bernadet	ALESSIO METHOD OF ISOLATING RESTRICTION DELETIONS IN VIBRIO CHOLERAE, AN		ZIE Avenue, N.				ble AMS-DOS	se #1.0, v	US/07/931,943	7/821.072		7/533,315	5/581,406	5/472.276		7/363,383	US 06/867,633	ç	223 BAMCZ0016P6 ON:	0			:
niz (Sch	ACCCAGTCGGCTTGCATCAAAGGCTCGGGGGGGGGGCTTGGTT	uwetThrphealagluglualathrph :::::::::       TGCTCCTATGTCGAGGAGTTTGGTTACAACCTCTGTTT		eq_name: /cgn2_6/ptodata/1/1na/5A_COMB.seq:US-0	on 05/0793	GENERAL INFORMATION:	KAPER, James B. BAUDRY-MAURELLI, Bernadette	-	ADDRESS:	ADDRESSEE: BAKER & NCKENZIE STREET: 815 Connecticut Avenue, N.W	g		PORM: OPPy disk	C compatii 1: PC-DOS,	- 2	MBER: US/07 19920812	DATA:	16-JAN-1992 ON DATA:	APPLICATION NUMBER: US 07/533,315 FILING DATE: 05-JUN-1990	DATA:	FILING DATE: 1/-FEB-1984 PRIOR APPLICATION DATA: 05/472.276 APPLICATION NUMBER: US 06/472.276	-MAR-1983 DATA:	APPLICATION NUMBER: US 07/363,383 FILING DATE: 05-JUN-1989 PRIOR APPLICATION DATE:	MBER: US 06 27-MAY-1986	ORMATION:	REGISTRATION NUMBER: 25,223 REFERENCE/DOCKET NUMBER: BA TELECOMMUNICATION INFORMATION:	(202) 452-7000 )2) 452-7074	OR SEQ ID NO: 1. IARACIERISTICS: 2912 base pairs	ACID double nown DNA (genomic)	
ThrVallaraThrLenHisGln	AGECGGCTT	uMethrPhealagluglu. : ::::::      Trgcrccrafccaggagr	202 euPherhr 204        :::    03 TCTTTTCT 1110	n2_6/ptoda	eq_documentation_block Sequence 1, Applicati	GENERAL INFORMATION:	APPLICANT: KAPER, APPLICANT: BAUDRY	25 25 (	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES	SEE: BAKE : 815 Con	CITY: Washington STATE: OC	Y: US 20006	COMPUTER READABLE PORM: MEDIUM TYPE: Floppy	ER: IBN P ING SYSTEM	RE: Paten APPLICATIO	APPLICATION NUMBER: FILING DATE: 19920	PRIOR APPLICATION 633 APPLICATION DATA: APPLICATION NUMBER: 1	FILING DATE: 16-JAN- PRIOR APPLICATION DATA:	ATION NUMB DATE: 05	APPLICATION DATA:	DATE: 1/ PLICATION ATION NUMB	FILING DATE: 04-MAR- PRIOR APPLICATION DATA:	ATION NUMB DATE: 05 PLICATION	APPLICATION NUMBER: FILING DATE: 27-MA	ATTORNEY/AGENT INFORMATION: NAME: Kile, Bradford E.	REGISTRATION NUMBER: 25 REFERENCE/DOCKET NUMBER: LECOMMUNICATION INFORMAT	TELEFANE: (202) TELEFAX: (202)	INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2912 base pairs	TYPE: NUCLEIC ACID STRANDEDNESS: double TOPOLOGY: unknown LECULE TYPE: DNA (GP	ORIGINAL SOURCE:
) 1	i – g	Sc. et	원드밝	55	1,	. 2	22	5695	2 6	問問	jä	COUNTRY: ZIP: 20	部屋	5£	ž E	ដទូដ	1 20 1	맞	ដូច្ន	AU:	E P C	28.2	NO A	ដូខ្ល	점	궁범즼	品品	납위품	TYPE: STRAND TOPOLO	Z

189 uMetThrPheAlaGluGlu..........AlaThrPheGluPheArgL 202

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1986 AGTIAGAAACGGCTCAGCAGAATITAAAGCAGATGATCAACGATAAAATC 2035
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                                                                                                                                                                                                                                    CITGAAGAAGTICGCAICGAIGTAIGGGAIACACAACGGGAGGICAGAAA 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1745 GCGATIGATGAGCTTAAAGATTCACTCGGTGGGGTTGTCGTTCCGCCTAA 1794
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F: Poulin, Matthew L
INVENTION: Acidic Fibroblast Growth Factor (aFGF)
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DDRESSEE: Ing-Ming Chiu
STREET: S2052 Davis Medical Research Center, 480 West
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                                         1525 AGATATGGTTCAGCTCAATAGGAAGTTTCACGGGGGCCGTGTTCTTGAAA
                                                                                       61 rqValAlaGluileAsnAlaAlaGlnAsnProAsnAsnGluValThrTyr
                                                                                                                                      1575 AAGTGAACGCAATCAAC.....AATCGATTGAATGGGCAGATAACTAT
                                                                                                                                                                                     78 LeuLeuProGinAlaile....
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easp1leSerLeuLeuGluAsn.....
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                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-624-601-1
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Percent Identity: 23.729
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1100 New York Ave. N.W. Suite 300 East
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US-09-151:189-2_COPY_441_676'x US-08-624-601-1
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Vibrio cholerae
TITLE OF INVENTION: (CVD112 and CVD1
TITLE OF INVENTION: of making same a
                                                                                                                                                                                                                              quence 1, Application US/08624601
cent No. 5882653
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1768 GAATACTTGGGCACCGGCGCCCACCTGGCATGGAGTACTCCTTTGAC.. 1815
                                        1421 ACTIGCIGGCCGGGGTCICCGAGIAIGAGCIGCCAGAGGACCCCAAGIGG 1470
                                                                                                                                        1471 GAGTATCCAAGGGAAAAGCTCACGCTGGGGAAGCCCCTGGGCGAAGGCTG 1520
                                                                                                                                                                                                                                 521 CTTCGGGCAGGTGGTGATGGCAGAGGCGGTGGGCATCGACAAGGACCGGC 1570
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F: Poulin, Matthew L
INVENTION: Additor Missophast Growth Factor (aFGF)
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77 yrleuLeuProGlnAlaileGlnValGlySerProThrHisPro.....
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S2052 Davis Medical Research Center, 480
9th Avenue
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1768 GAATACTIGGGCACCCGCGCGCCTGGCATGGAGTACTCCTTTGAC. 1815
1621 GAGAAGGATCTTTCTGATCTGGTGTCTGAGATGGAAATGATGAAGATGAT 1670
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Poulin, Matthew L
ENTION: Acidic Fibroblast Growth Factor (aFGF)
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$2052 Davis Medical Research Center, 480 West
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squence 9, Application US/06070165F
itent No. 5750365
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1471 GAGTATCCAAGGGAAAAGCTCACGCTGGGGAAGCCCCTGGGCGAAGGCTG 1520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1336 GTGTCTGCTGACTCCAGCTCTTCTATGAACTCCAACACTCCACTGGTGGGGG 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 SerTyrProSer......GlyHisAlaThrGlnAsnGlyAl 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 LeuAspAlaAspPheAspIleSerLeuLeuGluAsnAspGluLeuLeuLy
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Percent Identity: 22.277
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                                                                                                                                                                                                                                                                  No. 5925528ophthalmus viridescent
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US-09-151-189-2_COPY_441_676 x US-08-885-418-5
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0.833
44.554
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325..2511
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Percent Similarity:
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: Chiu, Ing-Ning
: Poulin, Matthew L
INVENTION: Acidic Fibroblast Growth Factor (aFGF)
                                                                                                                  1774 GAATACTIGGGCACCCGCCGCCCACCTGGCAIGGAGIACTCCTITGAC. 1821
                                                                                                                                                                                                            ..ATCAACAGAATTCCTG 1837
                                                                                                                                                                                                                                                                                                  1838 AAGAGCAGATGACCTTCAAGGACCTAGTGTCTTGCACGTACCAACTGGCC 1887
                                                                       159 ..........ArgGlaMetLeuGly1leHisTyrArgPheAspGl 170
                                                                                                                                                               170 yileGlnGlyLeuLeuLeuGlyGluThrIleThrValArgThrLeuHisG 187
                                                                                                                                                                                                                                                       187 inGluLeuMetThrPheAlaGluGluAlaThrPheGluPheArgLeuPhe 203
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-885-418-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atentIn Release #1.0, Version #1.25
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DEVELOPMENTAL STAGE: Adult
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Mesenchyme and Epithelium
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quence 9, Application US/08885418
tent No. 5925528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 luCysPheProAsnProVal.....PheProSerAspAspGlyLeu 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 LeuAspAlaAspPheAspIleSerLeuLeuGluAsnAspGluLeuLy 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9: FROM 1 TO 2681
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Percent Identity: 22.277
TISSUE TYPE: Regenerating forelimb blastema CELL TYPE: Mesenchyme and Epithelium
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US-09-151-189-2_COPY_441_676 x US-08-070-165F-9
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                                                                     lambda gtlI
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325..2517
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1..324
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                                                                             POSITION IN GENOME ONLY
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Ouality:
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Percent Similarity:
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JOURNAL:
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: tim cDNA sequence wherein R at position 1335
                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-619-198-2
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US-09-151-189-2_COPY_441_676 x US-08-619-198-2/rev
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1838 AAGAGCAGATGACCTTCAAGGACCTAGTGTCT
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quence 2, Application US/08619198
tent No. 5885831
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DIUM TYPE: Floppy
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Percent Similarity:
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US-08-885-418-9
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Percent Identity: 22.277
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US-09-151-189-2_COPY_441_676 x US-08-885-418-9
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             325..2517
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Percent Similarity:
                LOCATION:
                                                                                                                        PUBLICATION
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to: 3369

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im cDNA sequence wherein R at position 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AsnProValPheProSerAspAspGlyLeuGlu.LeuIleAsnPheGluG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 lyAlaCysLeuThrTyrGluGlyGluIleAsnLysLeuAlaValAsnVal 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 rTyrProSerGlyHisAlaThrGlnAsnGlyAlaPheAlaThrValLeuL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 ysAlaLeuIleGlyLeuAspArg...GlyGlyGluCysPhePro..... 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 AlaPheGlyArgGlnMetLeuGlyIleHisTyrArgPheAspGlyIleGl 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 ThrTyrLeuleuProGlaAlaIleGlaValGlySerProThrHisProSe 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/1na/5B_COMB.seq:US-08-399-561-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-619-198-4 from: 1
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US-09-151-189-2_COPY_441_676 x US-08-619-198-4/rev
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
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Quality:
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                                                                       2071 ACGTATCAATGGCCTGGA....GGAACTCCCGGATGGCCGTC 2034
                                                                                                                                                                                                                                                                                                                                     1014 :.....TTAGATAGGGCTTCAGGTCACTGCCCTCTGTCGGG 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1978 CATTCAGTTCCAGTTGCTCACATAGGGACACCCCTCATAGGTCAAGTAG 1929
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                                                                                                                                        92 rIyrProSerGlyHisAlaThrGlnAsnGlyAlaPheAlaThrValLeuL 109
                                                                                                                                                                                                                                                                                                                                                                                                     123 AsnProValPheProSerAspAspGlyLeuGlu.LeuIleAsnPheGluG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 lyAlaCysLeuThrTyrGluGlyGluIleAsnLysLeuAlaValAsnVal 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 n..... GlyLeuLeuLeuGlyGluThrIleThrValArgThrL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 euHisGlaGluLeuMetThrPheAlaGluGluAlaThrPheGluPheArg 201
76 ThrTyrLeuLeuProGlnAlaIleGlnValGlySerProThrHisProSe 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/1na/5C_COMB.seq:US-08-619-198-4
                                                                                                                                                                                                                                                                    109 ysAlaLeuIleGlyLeuAspArg...GlyGlyGluCysPhePro...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MBER: US/08/619,198
20-MAR-1996
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equence 4, Application US/08619198
atent No. 5885831
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                                                                                                                                                                                                        2033 ACCACCAAGT
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127 ProSerAspAspGlyLeuGluLeulleAsnPheGluGlyAlaCysLeuTh 143
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                             623 GAGTCGGAT.....TACTACAACTTCGAAGCC.....597
                                                                                      143 rTyrGluGlyGluIleAsnLysLeuAlaValAsnValAlaPheGlyArgG 160
                                                                                                                                                                       160 inMetLeuGlyIleHisTyrArgPheAspGlyIleGlnGlyLeuLeuLeu 176
                                                                                                                                                                                                              565 ACATGCAGGACACCTTCTACCTCACTGACGGC....AATCTGCTGCGC 522
                                                                                                              .::III ::: III ::: III ::: III ::: III ::: III
                                                                                                                                                                                                                                                                                                  521 ACTCACACATCGTCCGTGCAGATTCGCCACATGGAA 486
                                                                                                                                                                                                                                                        177 GlyGluThrIleThrValArgThrLeuHisGlnGlu 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGACACCTTCACCCGCTGCAAGCACGATCGATCGCATTCTCGACA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 ArgProGlualaLeuGlyGlyThrLeuHisAsnThrIleAlaGlyAspLe 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLeuProGlnAlaileGlnValGlySerProThrHisProSerTyrPr 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 uAspAlaAspPheAsplleSerLeuLeuGluAsnAspGluLeuLeuLysA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 rgValAlaGluIleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyr 77
                                                                                   6 Associates
5. 5792903thwestern Highway, Suite 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-08-399-561-1 from: 1
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Gaps: 12
Percent Identity: 29.630
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US-09-151-189-2_COPY_441_676 x US-08-399-561-1/rev
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  Gantt, Elisabeth
ENTION: Lycopene Cyclase Gene
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AA773086 ac2la08.sl
AII18935 ue22c04.yl
AIO48208 ud67902.yl
                                                                                                                                             sed_documentation_block:
LOCUS
LOCUS
AW400432
400 bp mRNA
DEFINITION Landisstl29est L.dlgltata sporophyte Lambda Zapli Laminarla
ACCESSION AW400432
ACCESSION AW400432
                                                                                                                                                                                                                                                                                                                                              group:
                                                                                                                                                                                                                                                                                             Laminaria digitata.
Laminaria digitata.
Laminaria digitata
Bukaryota; stramenopiles; Phaeophyceae/Xanthophyceae group
Phaeophyceae: Laminariales; Laminaria.

( hases 1 to 400)
Crepinaeulp., Roscoe, T., Kaas, R., Kloareg, B. and Boyen, C.
Characterisation of complementary DWAs from the Expressed
Tag analysis of life cycle stages of Laminaria digitata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Dec. 20, 1995 this sequence version replaced gi:1134035. On Dec. 20, 1995 this sequence version replaced gi:1134035. Other ESTs: Landisest129T7est contact: Boyen C Centre d'Etudes Oceanologique et de Biologie Marine. CNRS-LPR9042, Oniversite P. & M. Curie BP74, F-29682 Roscoff Cedex, France Teil: 33 2 98 29 23 32 Peil: 33 2 98 29 23 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 :IleGinGlyLeuLeuLeuGlyGluThrIleThrValArgThrLeuHisGl 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..........AlaThrPheGluPheArgLeuPheThrGlyGluV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 allleLysLeuPheGlnAspGlyThrPheSerIleAspGlyAspMetCys 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GIGTACGGAGCGCTCATGGGAGAGCCAGCTGCGTCGCCGCCTGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 78
Gaps: 3
Percent Identity: 33.333
                  503
510
547
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                  12.26
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US-09-151-189-2_COPY_441_676 x AW400432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@sb-roscoff.fr.
Location/Qualifiers
                  151.40
150.82
150.65
149.82
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                  74.00
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gb_est21:hA989777
gb_est19:hA4773086
gb_est23:A1118935
gb_est22:A1048208
                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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4 zw32f08.sl Soares over
5 FPG1-23-340Ell TV FPC1
51 SD05133.5prime SD Dros
23 tu54f04.xl NCI_CGAP_PT
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Sprime GH Dros
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71 Sommer Pris
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0 EST224515 Normalized r
4 qb63g01.xl NCI_CGAP_BI
T23N8TF TAMU Arabidopsis
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AL232282 BST228970 Normalized x
AL854183 UI-M-BHO-ajz-c-01-0-01
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yo77fil.ri
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mel7all.rl Soares mouse
8 Sheared DNA-lAll.rk Sh
yo77a04.rl Soares adult
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xb04b04.xl NCI_CGAP_Gt
mgie0002101f Rice blac
IMAJFV1_lm43al2.yl Lei
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                                                                                                                                                    -WODEL-frame+_pin_color=1 -DEV-x1p
-0-/cgn2_1/USPTO_spool/US09151189/runat_15052000_082512_1587/app_query.fasta.1
-DB-EST -CEMT-fastap -SUFFIX-441-676_rst_GAPOP-12.000
-GAPEXT-4.000 -MINMATCE-0.100 -LOOPEXT-0.000
-GAPEXT-4.000 -GAREXT-7.000 -YAPOP-10.000 -YAPDEXT-0.500
-GAPOP-6.000 -FGAPEXT-7.000 -YAPOP-10.000 -YAPEXT-0.500
-GAPOP-6.000 -FGAPEXT-7.000 -YAPOP-10.000 -YAPEXT-0.500
-TRANS-human40.cdl -LIST-45 -DOCALIGN-200 -THR_SCORE-pet
-ALIGN-15 -WODE-LOCAL -OUTFMT-Pfs -NORM-ext -MINIEN-0
-WAXELEN-1000000 -USER-GS09151189 -NCPU-6 -ICPU-3 -NO_XLPXX -WAIT
                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                  pfs
                  · out_format
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10.28
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11.73
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Ouery: 05-09-151-189-2_COPY_441_676
Ouery length: 236
Database: EST:*
Database sequences: 4857316
Database length: 2026611650
Search time (sec): 564.440000
           OM of: US-09-151-189-2_COPY_441_676
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gb_est23:AI151044
gb_gss3:B68016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est40:AW15510
gb_gss6:AQ849162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gss7:A0925191
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Crepineau, F., Roscoe, T., Kaas, R., Kloareg, B. and Boyen, C. Characterisation of complementary DNAs from the Expressed Sequence rag analysis of life cycle stages of Laminaria digitata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW4.01290 289 bp mRNA EST 07-FEB-2000 Lamdidest49lest L.dlgitata gametophyte Lambda Zapii Laminaria iiitata cDNA similar to vanadium bromoperoxidase, mRNA sequence
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Laminaria digitata!
Laminaria digitata
Eukaryote, stramanopiles; Phaeophyceae/Xanthophyceae group:
Phaeophycea: Laminariales; Laminariaceae; Laminaria.
1 (bases 1 to 289)
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other_EGTs: LandiGest491r7est
Contact: Boyen C
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CRRS-LERGOAZ, DIAVETSILE P. & M. Curle
BP74, P-29662 Roscoff Cedex, France
Tel: 37 2 98 29 23 32
Fex: 33 2 98 29 23 24
Email: estesb-roscoff.fr.
                                                                                                                                                                                                           122 .....TTTCTCTTAGAAGATGAGAACACATTCAGGAGATGCTGAAAGC 165
                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 TGCACCCCAGGTCACGTCTCCGGGC...CCTGAGCACCCAGAG..... 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 ulleGlyLeuAspArgGlyGlyGluCysPheProAsnProValPhePro. 127
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                                                                      95 ......CACCGACTGGAGAGTGCACGGCTTCGT.....121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 SerGlyHisAlaThrGlnAgnGlyAiaPheAlaThrValLeuLy8AlaLe 111
32 euglyGlyThrLeuHisAsnThrIleAlaGlyAspLeuAspAlaAspPhe 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 .....SerAspAspGlyLeuGluLeuIleAsnPheGluGlyAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 TAGCAGTGGGGGCTGGTGGCAGCGGCTGCAGCAGGGGGCC 403
                                                                                                                                                                                                                                                                                                                               49 AspileSerLeuLeuGluAspAsp......GluteuLeuLysAr
                                                                                                                                                                                                                                                                                  61 gValAlaGluIleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyrL
                                                                                                                                                                                                                                                                                                                                                                                                                               78 euLeuProGlnAlalleGlnValGlySerProThrHisProSerTyrPro
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AW401290.1 GI:6919794
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Please contact the R2PD: Ressourcensentrum, Heubnerweg 6, 14059
Berlin-Cherlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutherla; Primates; Catarrhini; Rominidae; Homo.
1 (bases 1 to 468)
Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiamann,S.
EST (Poustka, et al.)
Unpublished (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: poustka@mping-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DRF2); Email s.wiemann$ddxiz-heidelberg.de;
sequenced by DKF2 within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                               ALG45228
DKFZp434B2050_rl 434 (synonym: htes3) Bomo sapiens cDNA clone
NFZp434B2050_5', mRNA sequence.
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156 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1997 this sequence version replaced gi:2059563 Poustka A.J.
153 TTCTTGAGCTCTACGGCAGGAACTTGTACAAGCTGGACGACGAGCTTGTC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111111 :::||| :::||| 29 CACTACAGCAGCTCGTCGGGGGG..... 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 sTyrGlnLys .... .TrpGlnValHisArgPheAlaArgProGluAlaL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Innestrasse 73, 14195 Berlin, Germany Tel: +49-30-84131623 Fex: +49-30-64131128 Emmil: poustyae...
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Gaps: 9
Percent Identity: 28.859
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/clone_lib-"434 (synonym: htes3)"
/tissue_type-"testis"
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                                                                                                       224 SerGlyLeuValTyrThrGlyValAlaAspCys 234
                                                                                                                                                                          203 GAGGGG . GCCTTCACCGGCGACGACTTCTGT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="adul
/lab_host="DH10B
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AL045228.1 GI:5433390
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1.153
50.336
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US-09-151-189-2\_COPY\_441\_676 x AW400668

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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gaelse, J.S., Kucabar, T., Lacy, M., Lew, Martin, J., Morris, M., Schallenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Organ: gonad; Vector: pT7T3D-Pac (Pharmacia) with a ed polylinker: Site_1: Not I: Site_2: Eco RI: 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the modified pT7T3 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                  ui34b05.yl Soares mouse urogenital ridge NMUR Mus musculus cDicare IMAGE:1853169 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ikaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
therla; Rodentla; Sciurognathi; Muridae: Murinae; Mus.
(bases 1 to 480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA was ligated to Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Apr 13, 1988 this sequence version replaced gi:2958642.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Will WashU-HMI Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l ratio of male:female"

>e="urogenital ridge (embryonic)"

fetal, mixture of 11.5 and 12.5 dpc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Not I and Eco RI sites of the modified PTT
Library went through two rounds of normalizatio
constructed by Bento Soares and M.Fatima Bonaldo
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                                                                                    196 AlaThrPheGluPheArgLeuPheThrGlyGluValileLysLeuPheGl 212
                                                                                                                                                                     212 nAspGlyThrPheSerIleAspGlyAspMetCysSerGlyLeuValTyrT 229
                                                                                                                                                                                                             ... GCCTTCA 111
                                                                                                                           15 GCGACTTACAAATTCCGCCTTTACAGCGGTAAGATTCTTGAGCTCTACGG 64
                                                                                                                                                                                                             65 CAGGAACTTGTACAAGCTGGACGCCAAGCTCTGCGAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Washd-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466.
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                                            to: AW400668 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI316774.1 GI:4032041
                                                                                                                                                                                                                                                                                                 112 ccecceaceacrerer 128
                                                                                                                                                                                                                                                         229 hrGlyvalAlaAspCys 234
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                                                                                                                                                                                                                                                                                                                                                                                     seg_documentation_block:
LOCUS A1316774
DEFINITION U134b05.yl Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                            Align seg 1/1
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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ORIGIN
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Chracterisation of complementary DNAs from the Expressed Sequence
Tag analysis of life cycle stages of Laminaria digitata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roscoe and F Crepineau, was olio-(dT) primed and directionally cloned into a Uni-ZAPTM XR vector (Stratagene, la Jolla, CA, USA) using total mRNA from sprophytes harvested at 1/1e de Sieck (F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2000
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The Laminaria sporophyte library, contructed l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laminaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On May 9, 1996 this sequence version replaced gl:1301779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:80365"
clone_lib="L.digitata sporophyte Lambda ZaplI"
dev_stage="sporophyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               centre d'Etudes Oceanologique et de Biologie Marine CNRS-LPR9042, Universite P. & M. Curie BP74, F-25682 Roscoff cedex, France Fax: 33 2 98 29 23 34 Email: esta-
                                                                                                                                                                                                               196 AlaThrPheGluPheArgLeuPheThrGlyGluValIleLysLeuPheGl 212
                                                                                                                                                                                                                                                                                                    212 nAspGlyThrPheSerIleAspGlyAspMetCysSerGlyLeuValTyrT 229
                                                                                                                                                                                                                                                                                                                                              ..GCCTTCA 137
                                                                                                                                                                                                                                                         41 GCGACTTACAAATTCCGCCTTTACAGCGGTAAGATTCTTGAGCTCTACGG 90
                      39
                                                      Percent Identity: 35.897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism-"Laminaria digitata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s sporophyte vanadlum brom
                                                                                                                                                                                                                                                                                                                                              91 CAGGAACTIGIACAAGCIGGACGGCAAGCICIGCGAGGGG
                                                                                                                                                                     Align seg 1/1 to: AW401290 from: 1 to: 289
                                                                                                     allgnment_block:
US-09-151-189-2_COPY_441_676 x AW401290
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Location/Qualiflers
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Laminaria digitata
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                                                                                                                                                                                                                                                                                                                                                                                     229 hrGlyvalAlaAspCys 234
                                                                                                                                                                                                                                                                                                                                                                                                                               138 CCGGCGACGACTTCTGT 154
                                            2.726
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2.726
79.487
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Ratio: 2
Percent Similarity: 7
                      Quallty:
                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_Scores:
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allgament_scores
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ORIGIN
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KEYWORDS
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qb63g01.x1 NCI_CGAP_Brn23 Homo saplens cDNA clone IMAGE:1704916 similar to SW:NUBM_BOVIN P25708 NADH-UBIQUINONE OXIDOREDUCTASE 5 KD SUBGUNI PRECURSOR ;, mRNA sequence.
                                       /clone="RBRCM11"
/clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pr/713Pac; Site_l: EcoRI;
/incl="Organ: brain; Vector: pr/713Pac; Site_l: EcoRI;
/incl="Organ: brain; Vector: br/713Pac; Site_l: EcoRI;
// incl="Included rector brains" | 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Perinates; Catarrhlui; Hominidae; Homo.

1 (bases 1 to 470)

NCI/MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 AGTCCTTCTGGACGCTGTTCACGTGCTGCAAAATCTCTGACAAAACT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 IGGAAGICCGAIACCACCATCTCTCTCCCTCGCTCTGCCCATGGCCAAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 GlnValGlySerProThrHisProSerTyrProSerGlyHisAlaThrGl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 ATGCTCATGGGCAAACACCAGCATGTCCAGCCTCTTCAACATCTGAGCCA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 lyGlyGluCysPheProAsnProValPheProSerAspAspGlyLeuGlu 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 LeuileAsnPheGluGlyAlaCysLeuThrTyrGluGlyGluIleAsnLy 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 nAsnGlyAlaPheAlaThrValLeuLySAlaLeuIleGlyLeuAspArgG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 GCTTCCAGTACCTACA......AAAGAGGTACTGTCCATC.....C 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 ..........GGGTGTGCCACT......GG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 sLeualavalasnvalalapheGlyArgGlnMetLeuGlyIleH1sTyrA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 laAlaGlnAsnProAsnAsnGluValThrTyrLeuLeuProGlnAlaile 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 eSerLeuLeuGluAsnAspGluLeuLeuLysArgValAlaGluIleAsnA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 GlyThrLeuHisAsnThrIleAlaGlyAspLeuAspAlaAspPheAspIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: A1227820 from: 1 to: 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 ......TTCCCCAGCTCCATGGGACACGAAGATGAGGGCCTT
                                                                                                                                                                                                                                                                                                     Gaps: 6
Percent Identity: 23,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 GCATTGACCAGGTGAGGAAGGTCCTGGTAGGGGACGTTCTG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 rgPheAspGly1leGlnGlyLeuLeuLeuGlyGluThrIle 180
  /db_xref="ATCC (1nhost):2036189"
/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                              Length:
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US-09-151-189-2_COPY_441_676 x AI227820/rev
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LOCUS AI151044
DEFINITION qb63g01.x1 NC:
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Ratio:
Percent Similarity:
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EST224515 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
utheria; Rodentia; Sciurognathl; Muridae; Murinae; Rattus.
(Dases 1 to 673)
e. N.H. Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
erlavage,A.R. and Adama,M.D. of a Rat EST (REST) Catalog & Rat
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                                                                                                                                                                                                                                                                              381 CITCALGITACALCICAACCAAAICCAGAICCICATGIACACACACGCGG 332
                                                                                                                                                                                                                                                                                                                                                                                     331 GA......ACAGCCTGCCTGCCTGCCTGCTTCAGGGTGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                           97 .........HisAlaThrGlnAsnGlyAlaPheAlaThrValLeuLy 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 GAGGAACCAITACACAGCAGGAACTCTGCTGCTGCTGTCATATGCGTGCTGTCAG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 .LeuAspArgGlyGluCysPheProAsnProvalPheProSerAsp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .. 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 AspGlyLeuGluLeuIleAsnPheGluGlyAlaCysLeuThrTyrGlu.: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 CAGGGCTTCGAACTCGCGAACGCAGAG.....GTCCTTACTCAGGCGGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 .........GlyGlulleAsnLysLeuAlaValAsn.....v 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GACAGGGCTCCACGCCCACCGCTCCTAGGAGCCTCCCATCATGGTC 194
                                                                                                                                                                                                                                                                                                                                             81 lnAlalleGlnValGlySerProThrHlsProSerTyrProSerGly... 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 CICCIGGGGGGGGGGCCTGCACTGCCATAAGCCGAGGCCTCA 71
                                                                                                                                                                                                                                               65 IleAsnAlaAlaGlnAsnProAsnAsnGlu.ValThrTyrLeuLeuProG
                      Length: 126
Gaps: 9
Percent Identlty: 29.365
                                                                                                                                                                                               Align seg 1/1 to reverse of: AI316774 from: 1
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                                                                                                                    alignment_block:
US-09-151-189-2_COPY_441_676 x AI316774/rev
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/organlsm="Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 alalaPheGlyArgGlnMetLeuGly 163
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Seg primer: Ml3-21.
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Unpublished (1998)
Other_ESTS: TC63251
Contact: Lee, NR
                   83.50
1.246
53.175
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LOCUS A1227820
                      Quallty:
Ratio:
                                                                    Percent Similarity:
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allgnment_scores:
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KEYWORDS
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thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta:
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l (bases 1 to 616)
Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A BAC End Sequence patabase for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3
Unpublished (1997)
                                                                                                                                                                                                                       B68016 616 bp DNA GSS 09-DEC-1997 IZ3N8TF TAMU Arabidopsis thallana genomic clone IZ3N8, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: BeloBACII, Site_1: HindIII, Site_2: HindIII, Produced by Rod Wing": 141 c 132 g 183 t
330 CCAGICCACACCTCACGGNAIGGGGIACACTGGCCACAGCTITC...GI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566 ATTATGGGTGACTTGGATTTGGACTTTTATTATTCGGAAAGGAACGTTTT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 GCTCTGCAAATGAAAGATCCAGTTTGGGTTCTTGGATGTGGAAAAGTTA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Steve Rounsley
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
1918 818 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 .....AspIleSerLeuLeuGluAsnAspGluLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.50 Length: 114
1.310 Gaps: 55.263 (Percent Identity: 25.439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
                                                                                 to reverse of: B68016 from: 1
                                                      110 aleullediyLeuAspArgGlyGlyGluCysPhe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 liealaGiyAspLeuAspAlaAspPhe......
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US-09-151-189-2_CORY_441_676 x B68016/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex-Thermaphrodite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: (Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11b-"TAMO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rounsley@tigr.org
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                              B68016.1 GI:2666054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_GSSs: T23NBTR
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                                                                                                                                                                                                                                                                          urvey sequence.
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Locus B68016
                                                                                                                                                   seq_name: gb_gss3:B68016
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Percent Similarity:
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DEFINITION
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VERSION
KEYWORDS
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ORIGIN
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                                                                                                                                                                                                                                            Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP Clone distribution information can be
found through the I M.A.G.E. Consortium/LLML at:

www.blo.lini.gov/Dbrg/linge/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Pharmacia) with a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloned into
                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Not I and Eco R1 sites of the modified p1713 vector. Library is normalized, and was constructed by Bento Soares and M.Fatham Bonaldo."

136 c 122 g 114 t l others
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ified polylinker; Site_1: Not 1; Site_2: Eco R1; 1st
and cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                       CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not 1 and clo
                                                                    On Sep 12, 1996 this sequence version replaced gl:1404939.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
        Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP, PETGAP), Tumor Gene Index Impublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 resseccecescescerececerracaaaacescerraacerrerrar 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 AsnAspGluLeuLeuLysArgValAlaGluIleAsnAlaAlaGlnAsnPr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 oAsnAsnGluValThrTyrLeu......LeuProGlnAlalleGlnV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AlaArgProGluAlaLeuGlyGlyThr:LeuHisAsnThrIleAlaGlyA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 alGlySerProThrHisProSerTyrProSerGlyHis.....97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_INAGE:INGER:TOWN
/clone_lib=NcI_CGAP_BR03*
/tissue_type="gliobiastoma (pooled)"
/lab_host="DB10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.50 Length: 112
1.398 Gaps: 7
52.679 Percent Identity: 32.143
                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 947 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 187.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: All51044 from: 1 to: 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptors (Pharmacia),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-151-189-2_COPY_441_676 x All51044
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Percent Similarity:
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ORIGIN .
                                                      JOURNAL
COMMENT
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466 CTAAAATACAGAGGCTGGCTAAATCAATGCATAAGGTGGAAGTGAGGAA 417

Thu May 18 22:21:31 2000

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7 GlyAlaAlaGluLeuAlaGluArgAlaSerCys ... TyrGlnLysTrpGl 22
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Ludwig Institute for Cancer Research
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chol, W., Fang, E., Sasinowski, M., Wing, R. and Dean, R.A.,
Expressed sequence characterization during appressorium formation
in rice blast fungus, Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'dev_stage-"Germlnated conldla on appressorlum-inductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ascomycota: anamorphic Ascomycota; Pyricularia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI069032 796 bp mRNA EST 09-DEC-1999 mgae0005bA01f Magnaporthe grisea Appressorium Stage cDNA Library Pyricularia grisea cDNA clone mgae0005bA01f 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lone_llb='Magnaporthe grisea Appressorlum Stage cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jan 19, 1998 this sequence version replaced gl:2287141.
Contact: Dean,8.
Clemson Diversity Genomics Institute
Clemson University
100 Joxdan Hall, Clemson University
Tel: 864 556 5737
Fax: 864 656 4293
                                                         416 CGGAAGCTGCACTTCTTGTAGCACTACTGCTCACATCTGGGCCGGC 367
                                                                                                                    89 z......HisProSerTyrProSerGlyH1sAlaThrGlnAsnGlyAlaP 104
                                                                                                                                                                     366 ICITGGACATAACGGGTACTCGTCGGGTCATAGACTTGGGAATACCACT. 318
                                                                                                                                                                                                                  104 healaThrValLeuLysAlaLeuIleGlyLeuAspArgGlyGlyGluCys 120
                                                                                                                                                                                                                                                                      317 .....CGAAACAAATCTGGAAACTGT 297
                      73 AsnGluValThrTyrLeuLeuProGlnAlaIleGlnValGlySerProTh 89
                                                                                                                                                                                                                                                                                                                                                                    296 CITGGGAACCCATCAACACCTCAACATCGGGCTGCCATCTA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3 primer (AATTAACCCTCACTAAAGGG)
High quality sequence stop: 364.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   121 PheProAsnProValPheProSerAspAspGlyLeuGluLeu 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 22.596
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sert size of 1.5 kbp."
227 c 231 g 170 t
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lone-"mgae0005bA01f"
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US-09-151-189-2_COPY_441_676 x AI069032
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l (bases 1 to 796)
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Percent Similarity: 43.750
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TITLE
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AW179110 446 bp mRNA EST 16-NOV-1999
MR4-ST0066-190899-001-B02 ST0066 Homo saplens CDNA, mRNA sequence
AW179110
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Eukaryote, Metazoa, Chordata, Cranlata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhlal, Hominidae: Homo.

1 (bases 1 to 446)
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On Dec 20, 1995 this sequence version replaced gi:1134227
Contect: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 erProThrHisProSerTyrProSerGlyHisAlaThrGlnAsnGlyAla 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 ACCATTCCCGTCGGCTCTGGAACCCTTGGT......CGTATCATGAA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                      212 ......AAGCTCCCCCGATTCTTAACGCCTTGAGAC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 ......GIIICGCAACAICIGGCGAGAAIGICGIC 304
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68 GGGCCTCGCCTCGCTGCGCCCCAGCTTAAGACTCCCCAAATACTC 117
                                                                                                                                              118 TCTCGGTGCCAGGTTCGCCAGCACACAGGGTGTCGGTGATGGAAAGATTC 167
                                                                                                                                                                                                                 37 isasnihrilealaGlyaspleuaspalaAspPheaspileSerLeuLeu 53
                                                                                                                                                                                                                                                                                            168 ACCAGGTCATTGGTGCCGTCGTGGATGTGAAATTCGACACTGCC.....211
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                                                                           22 nVal...HisArgPheAlaArgProGluAlaLeuGly...GlyThrLeuH 37
                                                                                                                                                                                                                                                                                                                                                                   54 GluasnaspGluLeuLeuLysargValalaGluIleasnalaalaGlnas 70
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he PAPESP/LICR Human Cancer Genome Project
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata: Vertebrata, Mammalia,
Bukheria: Primates, Catarrhini: Hominidae, Eomo.

1. (bases 1 to 681)
Adams, M. D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J. C.
Use of human BAC EMG Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  paetics (info@resgen.com). BAC end search page:
.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                   GSS 20-APR-1999
genomic clone RPCI-11-52L19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-ll, For BAC
library availability, please centert nitting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 TGGTGCATCCATAAACCCTGAGCTAGACACAGAGTGCTGATTGGCGCATA 383
                       195 GlualathrPheGluPheArgLeuPheThrGlyGluValileLys.... 209
                                                     318 AIGGGCACAAIGGAIGGGCGIAICCIGCAGCIGGAGCICGGICACI 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....crccagcracacaraaagirc 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 uRisAspIhrileAlaGlyAspLeuAspAlaAspPheAspIleSerLeut 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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                                                                                                                         210 .....LeuPheGlnAspGlyThrPheSerIleAspGlyAsp 221
                                                                                                                                                                         368 AAACTACTIGCIGTAIGTCCAACTICTCACTG...GGTGAC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 30.631
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                                                                                                                                                                                                                                                                                                                                 sapiens
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US-09-151-189-2_COPY_441_675 x A0083529/rev
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/clone="RPCI-11-52L19"
                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS A0083529 681 bp DNA
DEFINITION RPCill+52L19.TJ RPCI-11 Homo
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                            Emall: asimpson@indwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=NR4&t2=MR4-ST0066-
190899-001-B02&t1=1999-08-19844=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               application
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Rua Prof. Antonio prudente 109, 4 andar, 01509-010, Sao paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: stomach, Vector: pucl8; Site_1: Smal; Site_2: Smal; A minh-library was made by cloning proderived from Organs FOR (U.S. Letters patent applic No. 196,716 - Ludwig Institute for Cancer Research) profiles into the BUC 18 Vector. Reverse transcript tissue mRNA and CDNA amplification were performed untlew stringency conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 GlyHisAlaThrGlnAsnGlyAlaPheAlaThrValLeuLySAlaLeuIl 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 GCCCTCCGGCGAGGCCTCGACTTCTTCCAGTCGCCCAGTTTTTGCCCCA 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 lAlaGluIleAsnAlaAlaGlnAsnProAsnAsnGluValThrTyrLeuL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 euProGlnAlalleGlnValGlySerProThrHisProSerTyrProSer 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 TICCCCATIGACCIGCTGGACACACTAATIGAIGAGGGIGTGGAGCGCTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 181
Gaps: 9
Percent Identity: 24.309
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db_xref="taxon:9606"
                                                                                                                                                                                                                                                      stop: 446.
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US-09-151-189-2_COPY_441_676 x AW179110
                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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High quality sequence stop:
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0.982
45.304
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Ratio:
Percent Similarity:
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ORIGIN
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LOCUS A1232282 618 bp mRNA EST 31-JAN-1999
DEFINITION EST228970 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
RKIB271 3' end, mRNA sequence.
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Eurheria; Redentia; Sclurognathi; Muridae; Murinae; Rattus.
1 (bases I to 618)
Lee, N.H., Glodek; A., Chandra, I., Mason, T.M., Quackenbush, J.,
Rerlavage, A.R. and Adams, M.D.
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9712, Medical Center Drive, Rockville, MD 20850, USA Tri . (301)-838-329 Fax: (301)-838-9208 Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                           121 heProAsnProValPheProSerAspAspGlyLeuGluLeuIleAsnPhe 137
                                                                                                                                                                                                                                                                                                                                302 .....ACCCAGCGACTCCCCCTTGTCAGTGCT 276
                                                                                                                                                                                                                                                                                                                                                                                   138 GludiyalacysjeuthrtyrGluGlyGluileAsnLysLeuAlaValAs 154
                                                                                                                                                                                                                                                                                                                                                                                                                                           275 GAGGGTGCCTGC......GCCCTGCCGTAGC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 nValalaPheGlyArgGlnMetLeuGlylleHlsTyrArgPheAspGlyI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 CATAGCCTTTGGGCCCATACTTCTTGCCGTA.....GCAGGAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 Leu.....HisglngludeumetthrPhealagluglualathrPh 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 CITCIIGCAGACCAIGCACAGGAAGCAGGAITIAIGGAAGCIGIIGCCII 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 eGluPheArgLeuPheThrGlyGluValIleLySLeuPheGlnAspGlyT 215
                                                        89 ThrHisProSer...TyrProSerGlyHisAlaThrGlnAsnGlyAlaPh 104
                                                                                                              386 ACACATGAGGCCTAATACAGGGTGGGGGAGAGAGGTTG 337
                                                                                                                                                                104 eAlaThrValLeuLysAlaLeuIleGlyLeuAspArgGlyGlyGluCysP 121
                                                                                                                                                                                                                  336 GGAGGGGATCTTTACTCACTCCTCGTGCTTGAT: .... 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 leGlnGlyLeuLeuLeu........GlyGluThrIleThrValArgThr 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 TIGCAGIAAATCICCICACCAIGCACGCCCACAGIGGIACIGICCAGAII 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AL120080 from: 1 to: 750
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/db_xref="ATCC (lnhost):2037931"
/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est24:AI232282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 hrPhe 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CATTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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This is the 5' sequence of the clone insert
Clone from S' Wienann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s wiemannédkfz- heidelberg. Ge;
sequenced by MediGenomix within the CDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcensentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL120080 750 bp mRNA EST 27-SEP-1999
DKF2P761M212_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DKF2P761M212 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ottenwaelder, B., Obermaler, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r: pSportl; Site_1: NotI; Site_2: SalI'
213 g 183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST (Ottenwaelder, et al.)
Unpublished (1989)
On Jun 22, 1988 this sequence version replaced g1:3247433.
Contact: Ottenwaelder B
                                                                                                                                                                   303 ACABACCCTGAGCTAGACACAGAGTGCTGCTGGCGCATACACAATCCTCC 254
                                                                                                                                                                                                                                                                              253 AGCC.....AGACATAAAAGTTCTCCAAGTCCCCACT 222
                                                                                                                                                                                                                                                                                                                                   98 laThrGlnAsnGlyAlaPheAlaThrValLeuLysAlaLeuIleGlyLeu 114
                                                                                                                                                                                                                                                                                                                                                                   53 euGluAsnAspGluLeuLysArgVal ...AlaGluIleAsnAlaAla 68
                                                                                                                                                                                                                        81 nAlaIleGlnValGlySerProThrHisProSerTyrProSerGlyHisA 98
                                                                                                              69 GlnAsnPro.....AsnAsnGluValThrTyrLeuLeu.....ProGl 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 78 50 Length: 135
Ratio: 1,172 Gaps: 1.77
Percent Similarity: 49.630 Percent Identity: 28.188
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/clone_lib-"761 (synonym: hamy2)"
/tlssue_type-"amygdala"
                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AspArgGlyGlyGluCysPheProAsnProVal 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 CCAGCGGGGCACGCCTGCACTCCTCAGCCCTTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-151-189-2_COPY_441_676 x AL120080/rev
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/db_xref="taxon:9606"
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This clon
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AUTHORS
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If Site_2: Eco Ri; Inc
s a subtracted library derived from
libraries from ten regions of the
hain stems, olfactory bulbs,
hain stems, olfactory bulbs,
                                                                                                                                                                                                                              Lab Clone distribution: NIH BWAP CDMA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BWAP cDMA clones, this record will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         normalized libraries of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with a modified
                                                                                                                                                                                  5-dT track served to identify it as a clonerebellum library CDNA Library Preparation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 ......LeuAspArgGlyGlyGlyGluCysPh@ProAsnProVal 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AAATTAAATCATCATCATGTTÄCATCTCAACCAAATCCAGATCCTCATGT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 GGTTCAGGGTGGGAGCAACCATTACACAGGAGGAACTCTGCTGCCCATAT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 aThrValLeuLysAla......leuIleGly.... 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 ccdrgcrgrcaggacaggccrccacgccacgcrcrrcraggagccr 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 PheProSerAspAspGlyLeuGluLeuIleAsnPheGluGlyAlaCysLe 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 yrLeuLeuProGlnAlaIleGlnValGlySerProThrHisProSerTyr 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ArgvalAlaGluileAsnAlaAlaGlnAsnProAsnAsnGlu.ValThrT .77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 others
                                                                                                                                                                                                                                                   is nor distribution of the BWAP cDNA clones, the accordingly when that means is determined Primer: Mil Forward
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US-09-151-189-2_COPY_441_676 x AI854183
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Percent Slmllarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1854183 498 bp mRNA EST 15-JUL-1999
1-M-BHO-ajz-c-01-0-UI.sl NIH_BMAP_M_S1 Mus musculus cDNA clone
1-M-BHO-ajz-c-01-0-UI 3', mRNA sequence.
                                              Site_1: EcoRI;
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Mus.
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On May 11, 1999 this sequence version replaced 91:4776633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GCAGCTGGGGACAAGAAAGAAAACCATTCCTGTTTCAGTCCAGGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614 CGAGGGGGAGAGCTGTGTCCAGGAGCCGTCACCATGTCGGAGAA...TT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 ly......GluIleAsnLysLeuAlaValAsnValAlaPheGly 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 yLeuLeuLeuGlyGluThrileThrvalArgThrLeuHlsGlnGluLeuM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 GluvalileLysLeu.....PheGlnAspGlyThrPheSerile. 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 etThrPheAlaGluGluAlaThrPheGluPheArgLeuPheThr ... Gly 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 .....GAATCCACCATTGTCTGTAACACCCTT....GACGGTA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 TCAGAGGTCAAGCTCACCCTTACCTTCCAAGACAAAGACTTCAAGGTGAC 295
                                              Vector: pT7T3Pac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 uGluLeulleAspPhe......GluGlyAlaCysLeuThrTyrGluG
                                                                                                                                                                                                                                                                                                                                                                                                                      116 ArgGlyGluCysPheProAsnProValPheProSerAspAspGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567 CGAGGICACAAACCIGAACAIGAAAICAGGGAIGTCCCIGAAGAITAAAG
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Percent Identity: 28.099
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US-09-151-189-2_COPY_441_676 x AI232282/rev
                clone_lib="Normalized
note="Organ: kldney; v
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'clone="RKIBZ71"
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57.025
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KEYWORDS
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to: 803

Gaps: 2 Percent Identity: 28.409

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225 AGTCCTTCTGGATGGTGCCACGTTTGCAGCACATCTCTGACAAAACT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 GlnValGlySerProThrHlaProSerTyrProSerGlyHlaAlaThrG1 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 nAsnGlyAlaPheAlaThrValLeuLysAlaLeuIleGly...LeuAspA 116
                                                                                                                                                                                                                                                     175 TGGAAGTCCGACACCACCATCCTCTCTCCTCACTCTGCCCATGGCCAAC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 ATGGTCATGGGCAAATACCAGCATGTCCAGCCCTTCAACATATGAGCCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GCTCATCATAACGGCCACAGTGAAAACAGCTCCATGGGACACAAGATG 26
                                                                                                                                                                                                                                                                                                              50 eSerLeuLeuGluAsnAspGluLeuLeuLysArgValAlaGlulleAsnA 67
                                                                                                                                                                                                                                                                                                                                                                                                          67 laAlaGlnAsnProAsnAsnGluValThrTyrLeuLeuProGlnAlaile 83
                                                                                                                                                                                                                        Align seg 1/1 to reverse of: Al304074 from: 1
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US-09-151-189-2_COPY_441_676 x AI304074/rev
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                          Ouality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                    A1304074 803 DP mRNA EST 08-DEC-1998 u163806 y1 Sugano mouse liver mlia Mus musculus CDNA cione LIMAGE:1887131 5' similar to TR:035678 035678 NONOGLYCERIDE LIPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rra, M., Hillier, L., Allen, M., Bowles, M., Dletrlch, N., Dubuque, T.
lael, S., Kucaba, T., Lacy, M., Le, M., Marth, J., Morrla, M.,
hellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pME18S-FL3; Site_1: Draili
CACCATGTG); 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouseest@watson.wustl.edu
lone is available royalty-free through LLNL; contact the
Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Mammalia;
Sclurognathi; Muridae; Murlnae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHMI Mouse EST Project
gton University School of MedicineP
orest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                   clone: similarity on wrong strand
142 uThrTyrGlu......GlyGlulleAsnLyaLeuAlaValA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .xref-"taxon:10090"
one-"IMAGE:1887131"
one_lib-"Sugano mouse liver mlia"
                                                                                                                                                       154 sn.....valAlaPheGlyArgGinMetLeuGiy 163
                                                                                                                                                                                                 370 GCCGAGGCCTCAGGTCCAGAGGCCGCCAGAGGTCGGG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: custom primer used
High quality sequence atop: 422.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washu-HHMI Mouse EST Project
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therla; Rodentla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reversed
                                                                                                                                                                                                                                                seq_name: gb_est25:AI304074
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Thu May 18 22:21:31 2000